

2 32
 CGA GTA AAT CGT TCT CGA AGC CTT AGT AAT AGC AAT CCA GAT ATA TCT GGG ACT CCC ACG
 arg val asn arg ser arg ser leu ser asn ser asn pro asp ile ser gly thr pro thr
 62 92
 TCA CCA GAT GAT GAA GTT CGA TCA ATC ATC GGG AGT AAG GGT TTA GAT CGC TCC AAT TCC
 ser pro asp asp glu val arg ser ile ile gly ser lys gly leu asp arg ser asn ser
 122 152
 TGG GTT AAC ACT GGT GGT CCA AAA GCT GCC CCA TGG GGA TCC AAC CCC AGT CCA AGT GCA
 trp val asn thr gly gly pro lys ala ala pro trp gly ser asn pro ser pro ser ala
 182 212
 GAA TCA ACA CAG GCT ATG GAT CGA AGT TGT AAT CGT ATG TCT TCG CAC ACA GAG ACG TCA
 glu ser thr gln ala met asp arg ser cys asn arg met ser ser his thr glu thr ser
 242 272
 AGT TTC TTA CAA ACA TTA ACG GGA CGC TTA CCA ACT AAA AAG CTT TTT CAC GAG GAG CTG
 ser phe leu gln thr leu thr gly arg leu pro thr lys lys leu phe his glu glu leu
 302 332
 GCT TTG CAG TGG GTT GTT TGC AGT GGC AGC GTT CGG GAA TCA GCT TTG CAA CAA GCC TGG
 ala leu gln trp val val cys ser gly ser val arg glu ser ala leu gln gln ala trp
 362 392
 TTC TTT TTT GAA TTA ATG GTA AAG AGC ATG GTG CAC CAT TTA TAC TTT AAT GAT AAA CTT
 phe phe phe glu leu met val lys ser met val his his leu tyr phe asn asp lys leu
 Cadherin
 422 |xxx cleavage xx| 452
 GAG GCT CCA AGG AAA AGT CGT TTT CCA GAA CGT TTC ATG GAT GAC ATT GCA GCT CTT GTC
 glu ala pro arg lys ser arg phe pro glu arg phe met asp asp ile ala ala leu val
 482 512
 AGC ACG ATT GCT AGT GAT ATA GTT TCA CGA TTT CAG AAG GAC ACA GAA ATG GTT GAG AGA
 ser thr ile ala ser asp ile val ser arg phe gln lys asp thr glu met val glu arg
 542 572
 CTC AAT ACA AGC CTT GCA TTC TTT CTC AAT GAT CTG TTG TCT GTT ATG GAC AGA GGA TTT
 leu asn thr ser leu ala phe phe leu asn asp leu leu ser val met asp arg gly phe
 602 632
 GTT TTT AGC CTT ATA AAG TCC TGC TAT AAA CAG GTG TCT TCA AAG CTT TAC TCA TTA CCG
 val phe ser leu ile lys ser cys tyr lys gln val ser ser lys leu tyr ser leu pro
 662 692
 AAT CCC AGT GTT CTG GTG TCC TTG AGG CTG GAT TTT CTA CGA ATC ATC TGC AGT CAT GAG
 asn pro ser val leu val ser leu arg leu asp phe leu arg ile ile cys ser his glu
 722 752
 CAC TAT GTT ACA TTA AAC TTA CCC TGC AGC TTA CTT ACT CCA CCT GCA TCT CCA TCA CCT
 his tyr val thr leu asn leu pro cys ser leu leu thr pro pro ala ser pro ser pro
 782 812
 TCT GTT TCT TCT GCA ACA TCT CAG AGT TCT GGA TTT TCT ACG AAT GTA CAA GAC CAA AAG
 ser val ser ser ala thr ser gln ser ser gly phe ser thr asn val gln asp gln lys
 842 872
 ATT GCA AAT ATG TTT GAA TTA TCC GTG CCT TTC CGC CAA CAG CAT TAT TTG GCA GGA CTT
 ile ala asn met phe glu leu ser val pro phe arg gln gln his tyr leu ala gly leu

FIG. 1 (1 of 5)

Cadherin

|xx EC motif xx|

932
 GTG TTA ACA GAG CTG GCT GTC ATT TTA gac cct gat gct gaa gga ctg TTT GGA TTG CAT
 val leu thr glu leu ala val ile leu asp pro asp ala glu gly leu phe gly leu his

962 992
 AAG AAA GTC ATC AAT ATG GTA CAC AAT TTA CTC TCC AGT CAC GAC TCA GAC CCG CGG TAC
 lys lys val ile asn met val his asn leu leu ser ser his asp ser asp pro arg tyr

1022 1052
 TCT GAC CCT CAG ATA AAG GCT CGA GTG GCC ATG TTG TAT CTA CCT CTG ATT GGT ATT ATC
 ser asp pro gln ile lys ala arg val ala met leu tyr leu pro leu ile gly ile ile

1082 1112
 ATG GAA ACT GTA CCT CAG CTG TAT GAT TTT ACA GAA ACT CAC AAT CAA CGA GGA AGA CCA
 met glu thr val pro gln leu tyr asp phe thr glu thr his asn gln arg gly arg pro

1142 1172
 ATT TGT ATA GCC ACT GAT GAT TAT GAA AGT GAG AGC GGA AGT ATG ATA AGC CAG ACC GTT
 ile cys ile ala thr asp asp tyr glu ser glu ser gly ser met ile ser gln thr val

1202 1232
 GCC ATG GCA ATC GCA GGG ACA TCG GTC CCT CAA CTA ACA AGG CCT GGC AGT TTC CTC CTC
 ala met ala ile ala gly thr ser val pro gln leu thr arg pro gly ser phe leu leu

1262 1292
 ACG TCA ACG AGT GGC AGG CAA CAC ACT ACC TTT TCA GCA GAA TCA AGT CGA AGC CTT TTG
 thr ser thr ser gly arg gln his thr thr phe ser ala glu ser ser arg ser leu leu

1322 1352
 ATC TGT CTA CTT TGG GTT CTC AAA AAT GCA GAT GAA ACA GTT CTA CAG AAG TGG TTT ACA
 ile cys leu leu trp val leu lys asn ala asp glu thr val leu gln lys trp phe thr

1382 1412
 GAT CTC TCA GTC TTG CAG CTA AAC CGG CTA TTA GAT CTG CTT TAT CTC TGT GTG TCT TGC
 asp leu ser val leu gln leu asn arg leu leu asp leu leu tyr leu cys val ser cys

1442 1472
 TTT GAG TAT AAA GGG AAA AAA GTG TTT GAA CGA ATG AAT AGC TTG ACC TTT AAG AAA TCA
 phe glu tyr lys gly lys lys val phe glu arg met asn ser leu thr phe lys lys ser

1502 1532
 AAA GAC ATG AGA GCA AAG CTT GAA GAA GCT ATT CTT GGG AGC ATA GGT GCC AGG CAA GAA
 lys asp met arg ala lys leu glu glu ala ile leu gly ser ile gly ala arg gln glu

1562 1592
 ATG GTA CGG CGA AGC CGA GGA CAG CTC GAG AGA AGC CCA TCT GGA AGT GCC TTT GGA AGT
 met val arg arg ser arg gly gln leu glu arg ser pro ser gly ser ala phe gly ser

1622 1652
 CAA GAA AAT TTG AGG TGG AGG AAA GAT ATG ACT CAC TGG CGT CAA AAC ACA GAG AAG CTT
 gln glu asn leu arg trp arg lys asp met thr his trp arg gln asn thr glu lys leu

1682 1712
 GAC AAA TCA AGA GCA GAG ATT GAA CAC GAA GCA CTG ATT GAT GGA AAC CTG GCT ACA GAA
 asp lys ser arg ala glu ile glu his glu ala leu ile asp gly asn leu ala thr glu

1742 1772
 GCA AAC CTA ATC ATT TTA GAT ACA TTA GAG ATT GTT GTT CAG ACC GTT TCT GTA ACG GAA
 ala asn leu ile ile leu asp thr leu glu ile val val gln thr val ser val thr glu

1802 1832
 TCC AAA GAG AGC ATT CTT GGT GGA GTG CTA AAA GTG CTA CTA CAC AGC ATG GCC TGT AAC
 ser lys glu ser ile leu gly gly val leu lys val leu leu his ser met ala cys asn

FIG. 1 (2 of 5)

1862
 CAA AGT GCA GTT TAT CTA CAA CAC TGT TTT GCT ACA CAG AGA GCC TTG GTT TCA AAG TTT
 gln ser ala val tyr leu gln his cys phe ala thr gln arg ala leu val ser lys phe

1892
 GCT ACA CAG AGA GCC TTG GTT TCA AAG TTT
 ala thr gln arg ala leu val ser lys phe

1922
 CCT GAA CTC TTA TTT GAA GAA GAG ACA GAG CAG TGT GCT GAT TTA TGC CTC AGG CTT CTC
 pro glu leu leu phe glu glu glu thr glu gln cys ala asp leu cys leu arg leu leu

1952
 CAG TGT GCT GAT TTA TGC CTC AGG CTT CTC
 gln cys ala asp leu cys leu arg leu leu

1982
 CGA CAC TGT AGC AGT AGC ATC GGT ACA ATA CGG TCA CAC CCC AGT GCC TCC CTT TAC CTA
 arg his cys ser ser ser ile gly thr ile arg ser his pro ser ala ser leu tyr leu

2012
 CGG TCA CAC CCC AGT GCC TCC CTT TAC CTA
 arg ser his pro ser ala ser leu tyr leu

2042
 CTA ATG AGG CAA AAC TTT GAG ATT GGG AAT AAC TTT GCC AGG GTT AAA ATG CAG GTA CCA
 leu met arg gln asn phe glu ile gly asn asn phe ala arg val lys met gln val pro

2072
 AAC TTT GCC AGG GTT AAA ATG CAG GTA CCA
 asn phe ala arg val lys met gln val pro

2102
 ATG TCA CTA TCC TCC TTG GTG GGC ACA TCT CAG AAT TTT AAT GAA GAA TTC TTA AGA CGT
 met ser leu ser ser leu val gly thr ser gln asn phe asn glu glu phe leu arg arg

2132
 CAG AAT TTT AAT GAA GAA TTC TTA AGA CGT
 gln asn phe asn glu glu phe leu arg arg

2162
 TCT CTA AAG ACT ATA TTG ACA TAT GCT GAA GAA GAT CTG GAA TTG AGG GAA ACA ACA TTT
 ser leu lys thr ile leu thr tyr ala glu glu asp leu glu leu arg glu thr thr phe

2192
 GAA GAT CTG GAA TTG AGG GAA ACA ACA TTT
 glu asp leu glu leu arg glu thr thr phe

2222
 CCT GAT CAG GTC CAG GAT CTG GTT TTC AAT CTC CAT ATG ATT CTT TCT GAT ACT GTG AAA
 pro asp gln val gln asp leu val phe asn leu his met ile leu ser asp thr val lys

2252
 CTC CAT ATG ATT CTT TCT GAT ACT GTG AAA
 leu his met ile leu ser asp thr val lys

2282
 ATG AAG GAA CAC CAG GAG GAT CCT GAA ATG TTG ATT GAT CTA ATG tac aga att gcc aag
 met lys glu his gln glu asp pro glu met leu ile asp leu met tyr arg ile ala lys

2312
 TTG ATT GAT CTA ATG tac aga att gcc aag
 leu ile asp leu met tyr arg ile ala lys

2342
 ggt tac CAG ACC TCT CCA GAT CTG CGA TTG ACC TGG TTG CAG AAC ATG GCA GGC AAG CAC
 gly tyr gln thr ser pro asp leu arg leu thr trp leu gln asn met ala gly lys his

2372
 ACC TGG TTG CAG AAC ATG GCA GGC AAG CAC
 thr trp leu gln asn met ala gly lys his

2402
 TCA GAA CGA AGC AAT CAT GCT GAA GCT GCA CAG TGT CTA GTC CAC TCA GCA GCA CTT GTT
 ser glu arg ser asn his ala glu ala ala gln cys leu val his ser ala ala leu val

|xxxxxxxxxxxxxxxxxxxxx transmembrane domain xxxxxxxxxxxxxxxxxxxxxxxx|

2492
 GCT GAA TAT TTG AGC ATG CTG GAG GAC CGG AAA TAT CTT CCT GTG GGA TGT GTA ACA TTT
 ala glu tyr leu ser met leu glu asp arg lys tyr leu pro val gly cys val thr phe

2522
 CAG AAT ATT TCA TCT AAT GTT TTA GAA GAA TCT GCG GTC TCA GAT GAT GTG GTA TCT CCA
 gln asn ile ser ser asn val leu glu glu ser ala val ser asp asp val val ser pro

2552
 TCT GCG GTC TCA GAT GAT GTG GTA TCT CCA
 ser ala val ser asp asp val val ser pro

2582
 GAT GAA GAA GGT ATC TGC TCT GGA AAA TAC TTT ACT GAG TCA GGA CTT GTG GGA TTA CTG
 asp glu glu gly ile cys ser gly lys tyr phe thr glu ser gly leu val gly leu leu

2612
 TTT ACT GAG TCA GGA CTT GTG GGA TTA CTG
 phe thr glu ser gly leu val gly leu leu

2642
 GAA CAA GCA GCT GCT TCC TTC TCT ATG GCT GGC ATG TAT GAA GCA GTT AAT GAA GTT TAC
 glu gln ala ala ala ser phe ser met ala gly met tyr glu ala val asn glu val tyr

2672
 GGC ATG TAT GAA GCA GTT AAT GAA GTT TAC
 gly met tyr glu ala val asn glu val tyr

|xxx ITAM xxxx|

2732
 AAA GTA CTT ATT CCT ATT CAT GAA GCT AAT CGG GAT GCA AAG AAA CTA TCC ACA ATT CAT
 lys val leu ile pro ile his glu ala asn arg asp ala lys lys leu ser thr ile his

2762
 GGT AAA CTT CAA GAA GCA TTC AGC AAA ATT GTT CAT CAG AGT ACT GGC TGG GAG CGG ATG
 gly lys leu gln glu ala phe ser lys ile val his gln ser thr gly trp glu arg met

2792
 GTT CAT CAG AGT ACT GGC TGG GAG CGG ATG
 val his gln ser thr gly trp glu arg met

FIG. 1 (3 of 5)

```

2822      |xxxxxx ITAM xxxxx|      2852
TTT GGC ACC TAT TTT CGT GTT GGT TTT TAT GGA ACC AAG TTC GGG GAT TTG GAT GAA CAA
phe gly thr tyr phe arg val gly phe tyr gly thr lys phe gly asp leu asp glu gln

2882      2912
GAA TTT GTT TAC AAG GAG CCT GCA ATA ACC AAA CTT GCA GAG ATA TCT CAC AGA TTG GAG
glu phe val tyr lys glu pro ala ile thr lys leu ala glu ile ser his arg leu glu

2942      2972
GGA TTT TAC GGA GAA AGA TTT GGA GAG GAT GTG GTT GAA GTA ATC AAA GAC TCT AAT CCT
gly phe tyr gly glu arg phe gly glu asp val val glu val ile lys asp ser asn pro

3002      3032
GTA GAC AAG TGT AAA TTA GAT CCT AAC AAG GCA TAT ATT CAG ATT ACC TAT GTG GAG CCA
val asp lys cys lys leu asp pro asn lys ala tyr ile gln ile thr tyr val glu pro

3062      3092
TAC TTT GAC ACA TAT GAG ATG AAG GAC AGA ATC ACC TAT TTC GAC AAA AAT TAC AAT CTT
tyr phe asp thr tyr glu met lys asp arg ile thr tyr phe asp lys asn tyr asn leu

3122      3152
CGT CGA TTC ATG TAC TGT ACA CCC TTT ACT TTA GAT GGC CGT GCC CAT GGG GAA CTT CAT
arg arg phe met tyr cys thr pro phe thr leu asp gly arg ala his gly glu leu his

3182      3212
GAA CAA TTC AAA AGG AAG ACC ATT CTG ACT ACG TCT CAT GCC TTT CCT TAT ATT AAA ACA
glu gln phe lys arg lys thr ile leu thr thr ser his ala phe pro tyr ile lys thr

3242      3272      |xxxxxxxxxxxxxxxxxxxxxxxxxxxx
AGG GTC AAT GTC ACT CAT AAA GAA GAG ATC ATC TTA ACA CCA ATT GAA GTT GCT ATT GAG
arg val asn val thr his lys glu glu ile ile leu thr pro ile glu val ala ile glu

xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx Coiled coil -1 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
GAC ATG CAG AAA AAG ACA CAG GAG TTG GCA TTT GCA ACA CAT CAG GAT CCC GCA GAC CCC
asp met gln lys lys thr gln glu leu ala phe ala thr his gln asp pro ala asp pro

xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx|      3392
AAA ATG CTT CAG ATG GTA CTC CAG GGA TCT GTA GGC ACC ACA GTG AAT CAG GGG CCT TTG
lys met leu gln met val leu gln gly ser val gly thr thr val asn gln gly pro leu

3422      3452
GAA GTT GCC CAG GTT TTT CTG TCT GAA ATA CCT AGT GAC CCA AAG CTC TTC AGA CAT CAT
glu val ala gln val phe leu ser glu ile pro ser asp pro lys leu phe arg his his

3482      3512      |xxxxxxxxxxxxx
AAT AAA CTG CGA CTC TGC TTT AAA GAT TTT ACT AAA AGG TGT GAA GAT GCC TTA AGA AAA
asn lys leu arg leu cys phe lys asp phe thr lys arg cys glu asp ala leu arg lys

xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx Coiled coil 2 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx|
AAT AAG AGC TTA ATT GGG CCG GTT CAA AAG GAG TAT CAA AGG GAA TTG GGG AAA CTA TCT
asn lys ser leu ile gly pro val gln lys glu tyr gln arg glu leu gly lys leu ser

3602      3632
TCG CCT TAA AGA GGC CCT ACA GCC CTA GAT CAC AGA AAG TCC CTC AGT TAT CCA AGC CAG
ser pro STP

3662      3692
TAT TGC TTG TCC CCT GCC ACA GAG ATT CCT TCA GTC GAA TGA GCT TTC GCA AAA TGG ATC

3722      3752
TCT AAA CTG AAT GCA CTT GTT TTA TTC ATC TGC AAA GAG CCA TGT ATT CAA CAT CGA GTG

3782      3812
TGA AAA GAT CTA TTG GAA ACC AAC ATG GAA TGG AAT TCT GGA AAT TAT TAT TCA TTG AAG

```

FIG. 1 (4 of 5)

3842		3872
AAT GCA GTG GCC AAG AAA ATA TCA AAT GTA		GAT TGT TAA CGC TTG AGA ATC ATG GCT ATG
3902		3932
GTT TCT AAT GTT CGG GTA ACA AGC TGT TAT		CTT TTA AGA CAT TTT AAT GAC TCA AAG GTA
3962		3992
CAC TAT ACA TTT ACC ATT ATT TAT ACC ATA		GCT AAG GTT AAA AAT TTA TTC ACT TTA AGT
4022		4052
TCG TAT TTT TTA ATT TAT ATC ACC ATT TAT		AGA TTC ATT TTG GAC CCA TTT TAA ATG TAG
4082		4112
TAA TGC TTA TTT TAA AGG TAC TAA AAA ATA		TGT GAA TGT TTA CCT CGT GCG CGC CAG GGC
4142		
CTC		

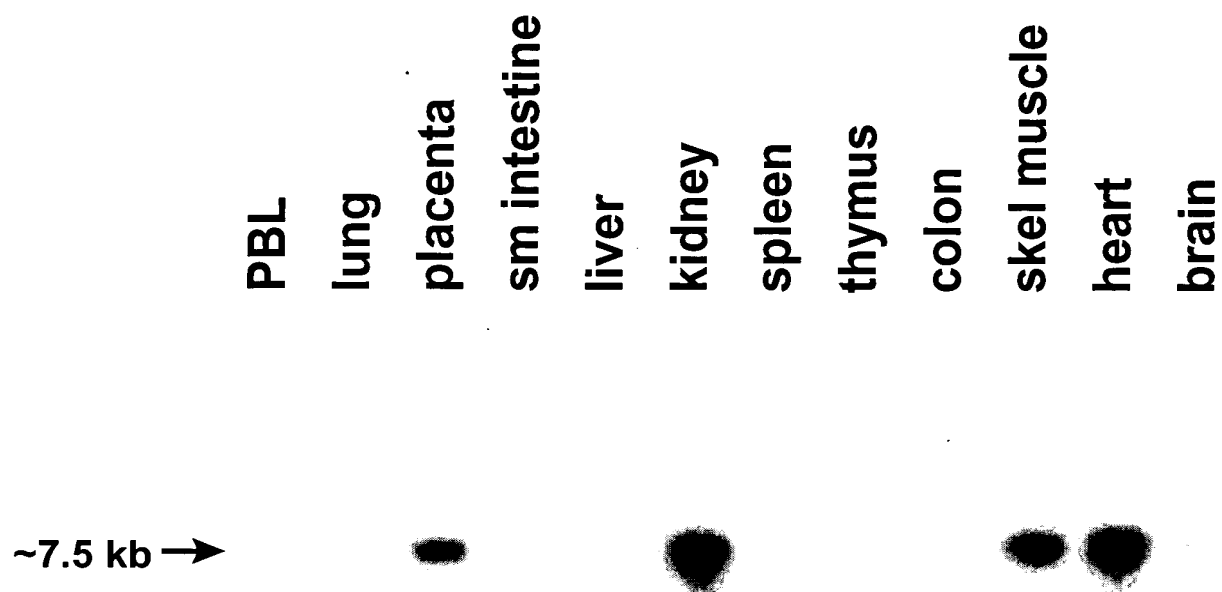


FIG. 2A

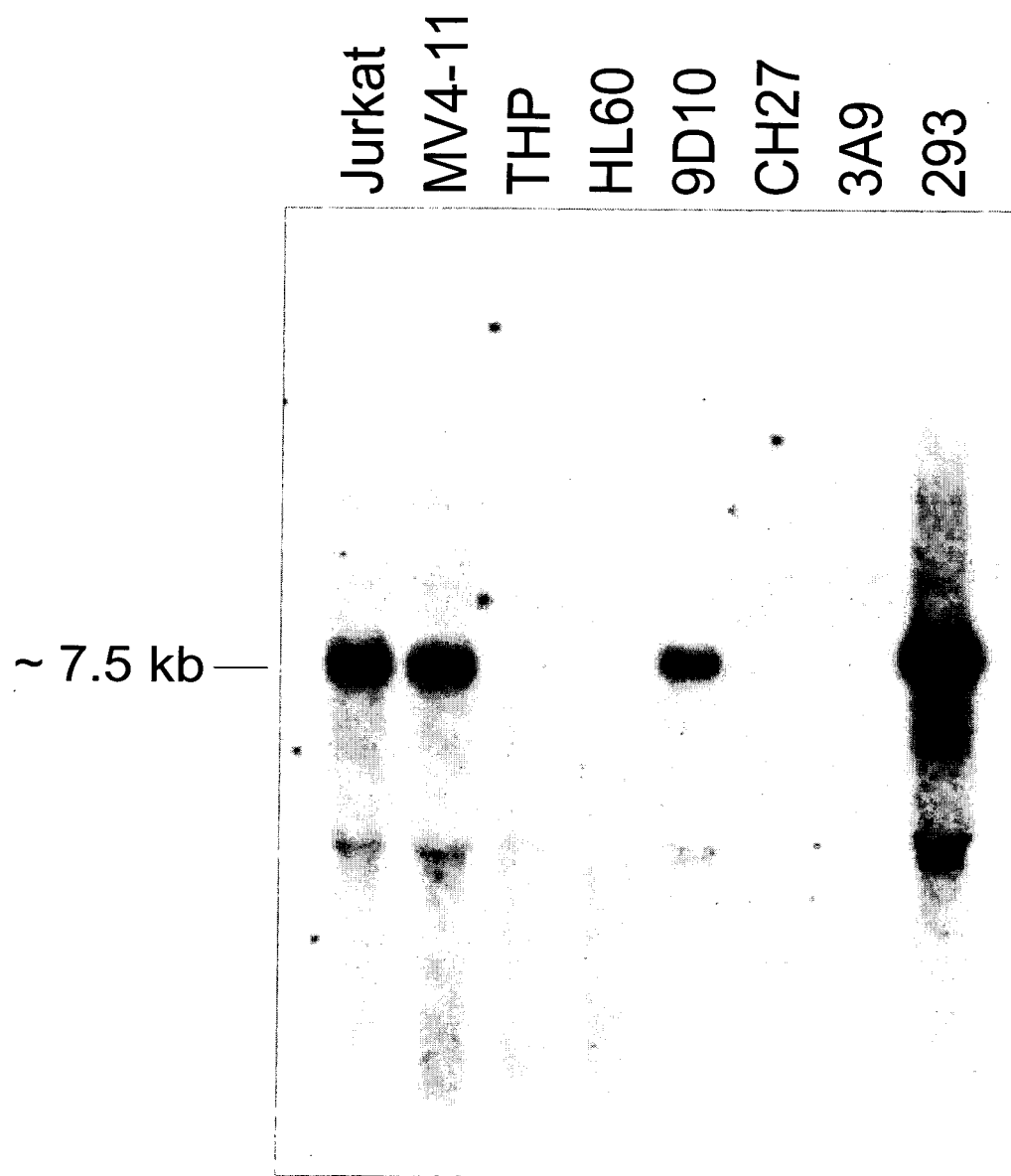


FIG. 2B

HC2A	-----
KIAA	ASGNLDKNARFSAIYRQDSNKLSDNDMLKLLADFRKPEKMAKLPVILGNLDITIDNVSSD
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	-----
KIAA	FPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKHTQPYTIYTNHLYVPKYLYKYSQ
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	-----VLHHHQNPFEYDEIK
KIAA	KSFAKARNIAICIEFKDSDEEDSQPLKCIYGRPGGPVFTRSAAFAVLHHHQNPFEYDEIK
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	IELPTQLHEKHHLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
KIAA	IELPTQLHEKHHLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	PVSANLPSGYLGQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNNFFQYC
KIAA	PVSANLPSGYLGQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNNFFQYC
rat	-----
HC4	-----
HC1	-----
HC3	-----GPGPARSTVSISLISNSARV
HC5	-----
HC2A	QKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV
KIAA	QKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV
rat	-----
HC4	-----MEIQVLIRFLSVILMQLFWVLPNMIHEDDVPISCPMV
HC1	-----MSFLPIILNQLFKVLV-QNEEDEITTTVTRV
HC3	NRSRSLSNSNPDISGTPTSPDDEVRSIIGSKGLDRSNSWVNTGGPKAAPWGSNPSPSAES
HC5	-----
HC2A	IIHVVAQCHEEGLESHLRSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSN
KIAA	IIHVVAQCHEEGLESHLRSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSN
rat	-----
HC4	LFHIVSKCHEEGLDSYLSSFIKYSFRPGKPSAPQAPLIHETLATMMIALKQSAFLAIN
HC1	LPDIVAKCHEEQLDHSVQSYIKFVFKTR---ACKERPVEDLAKNVTGLLK-SNDSPTVK
HC3	TQAMDRSCNRMSSHTETSSFLQTLTGRLP---TKKLFHEELALQWVVCSG--SVR---E
HC5	-----

FIG. 3A (1 of 5)

	Cadherin Cleavage
HC2A	KLLRYSWFFFDVLIKSMQHLIENSKVKLLRNQRFPPASYHHAAETVVNMLMPHITQKFGD
KIAA	KLLKYSWFFFDVLIKSMQHLIENSKVKLLRNQRFPPASYHHAAETVVNMLMPHITQKFRD
rat	-----
HC4	KLLKYSWFFFEIIAKSMATYLLLEENKIKLTHGQRFPPKAYHHALHSLFLAIT-IVESQYAE
HC1	HVLKHSWFFFAIILKSMQHLIDTNKIQLPRPQRFPPESYQNELDNLMVLSHDHVIWKYKD
HC3	SALQQAWFFFEELMVKSMVHHLYFNDKLEAPRKSRRPFRFMDDIAALVSTIASDIVSRFQK
HC5	-----
HC2A	NPEASKNANHSLAVFIKRCFTFMDRGFVFKQIN---NYIS--CFAPGDPKTLFEYKFEFL
KIAA	NPEASKNANHSLAVFIKRCFTFMDRGFVFKQIN---NYIS--CFAPGDPKTLFEYKFEFL
rat	-----
HC4	IPKESRNVNYSLASFLKCCLTLMDRGFVFNLIN---DYIS--GFSPKDPKVLAEYKFEFL
HC1	ALEETRRATHSVARFLKRCFTFMDRGCVFKMVN---NYIS--MFSSGDLKTLQYKFDL
HC3	DTMVERLNTSLAFFLNDLLSVMDRGFVFSLIKSCYQVSSKLYSLPNPSVLVSLRLDFL
HC5	-----
HC2A	RVVCNHEHYIPLNLP-----PFGKGRIQR-----YQDLQL----DYSLTDEF
KIAA	RVVCNHEHYIPLNLP-----PFGKGRIQR-----YQDLQL----DYSLTDEF
rat	-----
HC4	QTICNHEHYIPLNLP-----AFAKPKLQR-----VQDSNL----EYSLSDEY
HC1	QEVCOHEHFIPCLPIRSANIPDPLTPSES-----TQELHASDMPEYSVTNEF
HC3	RIICSHHYVTNLNLPCLSLTPPASPPSPSVSSATSQSSGFSTNVQDQKIANMFELS--VPF
HC5	-----MNADTAPTSPCPSIS---SQNSSSCSSFQDQKIASMFDRTSRVPA
	Cadherin EC motif
HC2A	CRNHFLVGLLLREVGTALQEFRE----VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT
KIAA	CRNHFLVGLLLREVGTALQEFRE----VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT
rat	-----
HC4	CKHHFLVGLLLRETSIALQDNYE----IRYTAISVIKNLLIKHAFDTRYQHKNQQAQIAQ
HC1	CRKHFLIGILLREVGFALQEDQD----VRHLALAVLKNLMAKHSFDDRYEPRKQAQIAS
HC3	RQQHYLAGLVLTTELAVILDPDAEGLFGLHKKVINMVHNLSSHSDPRYSDPQIKARVAM
HC5	SSTS-SPGLLFTELAAALDAEGEGISEVQRKAVSAIHSLLSSHDLDPRCVKPEVKVKIAA
HC2A	LYLPLFGLLIENVRQINVRDVSPFPVNAG-MTVKDESLALPAVNPLVTPQKGSTLDNSLH
KIAA	LYLPLFGLLIENVRQINVRDVSPFPVNAG-MTVKDESLALPAVNPLVTPQKGSTLDNSLH
rat	-----
HC4	LYLPPFVGLLLENIQRLAGRDITLYSCAAMPNSASRDEFPCG-----FTSP--AN--RGSLS
HC1	LYMPLYGMLLDNMPRIYLDLYPFTVNTSNQGSRDDLTNGGFQSQTAIKHANSVDTSFS
HC3	LYLPLIGIIMETVPQLYDFTETHNQGRPICIAATDDYESE-----SG---SMIS
HC5	LYLPLVGIILDALPQLCDFTVADTRRYR---TSGSDEEQE-----GA---GAIT
HC2A	KDLLGAISGIASPYTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQSS
KIAA	KDLLGAISGIASPYTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQSS
rat	-----
HC4	TDKDTAYGSFQNG-----HGIKREDSRGSLIP-EGATGFPDQGNLTGEN-----TRQS
HC1	KDVLNSIAAFSS-----IAISTVNHADSRASLASLDSNPSTNEKSSEKTDNCEKIPRL
HC3	QTVAMAIAGTSVPQ-----LTPRGSFLLTSTSGRQHT-----
HC5	QNVALAIAGNFNF-----LKTSG-IVLSSSLPYKQYN-----
HC2A	TLGNSVVRCDKLDQSEIKSLLMCFLYILKSMDDALFTYWN-KASTSELMDDFTISEVCL
KIAA	TLGNSVVRCDKLDQSEIKSLLMCFLYILKSMDDALFTYWN-KASTSELMDDFTISEVCL
rat	-----
HC4	STRSSVSQYNRLDQYBIRSLLMCYLYIVKMISEDITLLTYWN-KVSPQELINILILLEVCL
HC1	ALIGSTLRFDRLDQAETRSLLMCFHIMKTISYETLIAYWQ-RAPSPVSDFFSILDVCL
HC3	-----TFSAESSRSLICLLWVLKN-ADETVLQKWFTDLSVLQLNRLDLLLYLCV
HC5	-----MLNADTTRNLMICFLWIMKN-ADQSLIRKWIADLPSTQLNRILDLLFICV

FIG. 3A (2 of 5)

HC2A	HQFQYMGKRYIARNQEGLG--PIVHDRKS-----QTLPVSRNRTGMM
KIAA	HQFQYMGKRYIAR-----TGMM
rat	-----
HC4	FHFRYMGKRNIARVHDAWLSKHFGIDRKS-----QTMPALNRNSGVM
HC1	QNFRLYLGKRNIIRKIAAAF--KFVQSTQNNNGTLKGSNPSCQTSGLLAQWMHSTSRHEGHK
HC3	SCFEYKGGKVFERMNSLTFK--KSKDMRAK-----LEEAILGSIGARQEMV
HC5	LCFEYKGGKQSSDKVSTQVLQ--KSRDVKAR-----LEEALLRGEARGEMM

HC2A	HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC
KIAA	HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC
rat	-----
HC4	QARLQHL-----SSLESS-----FTLNHSSTTTEADIFHQALLEGNTATEVS
HC1	QHRSQTLPIIRGK---NALSNPKL---LQMLDNTMTSNSNEIDIVHHVDTEANITEGC
HC3	RRSRGQLERSPSGSAFGSQENLRWRKDMTHWRQNTTEKLDKSRAEIEHEALIDGNLATEAN
HC5	RRRAPGNDRFP----GLNENLRWKKEQTHWRQANEKLDKTKAELDQEALISGNLATEAH

HC2A	LTALDTLSLFTLAFKNQLLADHGHNPMLKKVFDVYLCFLQKHQSETALKNVFTALRSLIY
KIAA	LTALDTLSLFTLAFKNQLLADHGHNPMLKKVFDVYLCFLQKHQSETALKNVFTALRSLIY
rat	-----KLSRGHSPMLKKVFDVYLCFLQKHQSEMAKNVFTALRSLIY
HC4	LTVLDTISFFTQCFKTHFLNNDGHNPMLKKVFDIHLAFLKNGQSEVSLKHVFASIRAFIS
HC1	LTILDVLSLFTQTHQRQLQQCDCQNSLMKRGFDTYMLFFQVQNQSATALKHVFASLRLFVC
HC3	LIILDTLEIVVQTVS--VTES--KESILGGVLKVLLHSMACNQSAVYLQHCFAQRALVS
HC5	LIILDMQENIIQASS--ALDC--KDSLLGGVLRVVLVNSLNCDSSTTYLTHCFATLRALIA

HC2A	KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH
KIAA	KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH
rat	KFPSTFYEGRADMCASLCYEVLKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH
HC4	KFPSAFFKGRVNMCAAFCYEVLKCCTSKISSRNEASALLYLLMRNNFEYTKRKTFLRTH
HC1	KFPSAFFQGPADLCGSFCYEVLKCCNHRSRSTQTEASALLYLFMRKNFEPFNKQKSIVRSH
HC3	KFPELLFEEETEQCADLCRLRLRHCCSSSIGTIRSHPSASLYLLMRQNFIGN--NFARVK
HC5	KFGDLLFEEVEVEQCFDLCHQVLHHCSSSMDVTRSQCACATLYLLMRFSFGATS--NFARVK

HC2A	LQVIIISVSQLIADVVGIGETRFOQSLSIINNANCANDRLIKHTSFSSDVKDLTKRIRTVLM
KIAA	LQVIIISVSQLIADVVGIGETRFOQSLSIINNANCANDRLIKHTSFSSDVKDLTKRIRTVLM
rat	LQVIIISLSQLIADVVGIGETRFOQSLSIINNANCANDRLIKHTSFSSDVKDLTKRIRTVLM
HC4	LQIIIAVSQLIADVALSGGSRFOESLFIINNFANSRPMRLARAFPAEVKDLTKRIRTVLM
HC1	LQLIKAVSQLIAD-AGIGGSRFOHSLAITNNFANGDKQMKNSNFPFAEVKDLTKRIRTVLM
HC3	MQVPMSLSSLVGTSQNFNEEFLRRSLKTLITYAEEDLELRETTFPDQVQDLVFNLMHILS
HC5	MQVTMSLASLVGRAPDFNEEHLRRSLRILAYSEEDTAMQMTPFPTQVEELLCNLSILY

Transmembrane

HC2A	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLDSDMAIRHVKNGD	LSEAAMCYVHV
KIAA	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLDSDMAIRHVKNGD	LSEAAMCYVHV
rat	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLDSDMAIRHVKNGD	LSEAAMCYVHV
HC4	ATAQMKEHEKDPEMLIDLQYSLAKSYASTPELRKTWLDSDMAIRHVKNGD	LSEAAMCYVHV
HC1	ATAQMKEHEKDPEMLVDLQYSLANSYASTPELRRTWLESMAKIHARNGD	LSEAAMCYIHI
HC3	DTVKMKEHQEDPEMLIDLMYRIAKGYQTSDDLRLTLWLNMAAGKHSERSN	HAEAAQCLVHS
HC5	DTVKMREFQEDPEMLMDLMYRIAKSYQASDDLRLTLWLNMAEKHTKKKC	YTEAMCLVHA

		SH3	
HC2A	TALVAEYL	TRKGV-----	FRQGCTAFRVITPN
KIAA	TALVAEYL	TRKEA-----	VQWEPPLLPHSHSACLRRSRGGVFRQGCTAFRVITPN
rat	TALVAEYL	TRKEAD-----	LALQREPPVFPYSHTSCQRKSRGGMFRQGCTAFRVITPN
HC4	AALVAEFL	HRKKL-----	FPNGCSAFKKITPN
HC1	AALIAEYL	KRKGWYKVEKICTASLLSEDTHPCDNSLLTTPSGGSMFSMGWPAFLSITPN	
HC3	AALVAEYL	SMLLED-----	RKYLPGVCVTFQNISSN
HC5	AALVAEYL	SMLLED-----	HSYLPVGSVSFQNISSN

FIG. 3A (3 of 5)

HC2A	HQFQYMGKRYIARNQEGLG--PIVHDRKS-----QTLPVSRNRTGMM
KIAA	HQFQYMGKRYIAR-----TGMM
rat	-----
HC4	FHFRYMGKRNIARVHDAWLSKHFGIDRKS-----QTMPALNRNSGV
HC1	QNFRYLGKRNIIRKIAAAF--KFVQSTQNNGTLKGSNPSCQTSGLLAQWMHSTSRHEGKH
HC3	SCFEYKGGKVFERMNSLTFK--KSKDMRAK-----LEEAILGSIGARQEMV
HC5	LCFEYKGGKQSSDKVSTQVLQ--KSRDVKAR-----LEEALLRGEARGEMM

HC2A	HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC
KIAA	HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC
rat	-----
HC4	QARLQHL-----SSLESS-----FTLNHSSTTTEADIFHQALLEGNTATEVS
HC1	QHRSQLPIIRGK--NALSNPKL---LQMLDNTMTSNSNEIDIVHHVDTEANIATEGC
HC3	RRSRGQLERSPSGSFAFGSQENLRWRKDMTHWRQNTTEKLDKSRAEIEHEALIDGNLATEAN
HC5	RRRAPGNDRFP----GLNENLRWKKEQTHWRQANEKLDKTKAELDQEALISGNLATEAH

HC2A	LTALDTLSLFTLAFKNQLLADHGHNPMLKKVFDVYLCFLQKHQSETALKNVFTALRSLIY
KIAA	LTALDTLSLFTLAFKNQLLADHGHNPMLKKVFDVYLCFLQKHQSETALKNVFTALRSLIY
rat	-----KLSRGHSPLMKKVFDVYLCFLQKHQSEMAKKNVFTALRSLIY
HC4	LTVLDTISFFTQCFKTHFLNNDGHNPMLKKVFDIHLAFLKNGQSEVSLKHVFASLRAFIS
HC1	LTILDLVSLFTQTHQRQLQCCDCQNSLMKRGFDTYMLFFQVQNSATALKHVFASLRLFVC
HC3	LIILDTLEIVVQTVS--VTES--KESILGGVLKVLHSMACNSAVYLQHC FATQRALVS
HC5	LIILDMQENIIQASS--ALDC--KDSLLGGVLRVLVNSLNCDSSTTYLTHCFATLRALIA

HC2A	KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH
KIAA	KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH
rat	KFPSTFYEGRADMCASLCYEVLKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH
HC4	KFPSAFFKGRVNMCAAFCYEVLKCCCTSKISSRNEASALLYLLMRNNFEYTKRKTFLRTH
HC1	KFPSAFFQGPADLCGSFCYEVLKCCNHRSRSTQTEASALLYLFMRKNFEFNKQKSIVRSH
HC3	KFPELLFEEETEQCADLCLRLLRHCSSSIGTIRSHPSASLYLLMRQNFEIGN--NFARVK
HC5	KFGDLLFEEVEVEQCFDLCHQVLHHCSSSMDVTRSQCATLYLLMRFSFGATS--NFARVK

HC2A	LQVIISVSQLIADVVGIGETRFOQSLSIINNANCSDRLIKHTSFSSDVKDLTKRIRTVLM
KIAA	LQVIISVSQLIADVVGIGETRFOQSLSIINNANCSDRLIKHTSFSSDVKDLTKRIRTVLM
rat	LQVIISLSQLIADVVGIGETRFOQSLSIINNANCSDRLIKHTSFSSDVKDLTKRIRTVLM
HC4	LQIIIAVSQLIADVALSGGSRFQESLFIINNFANSRPLARAFPAEVKDLTKRIRTVLM
HC1	LQLIKAVSQLIAD-AGIGGSRFQHSALITNNFANGDKQMKNSNFPAEVKDLTKRIRTVLM
HC3	MQVPMSSLSSLVGTSQNFNEEFLRRSLKTIITYAEEDLELRETTFPDQVQDLVFNLMILS
HC5	MQVTMSLASLVGRAPDFNEEHLRRSLRITILAYSEEDTAMQMPFPPTQVEELCNLSILY

Transmembrane

HC2A	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKNGD	LSEAAMCYVHV
KIAA	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKNGD	LSEAAMCYVHV
rat	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKNGD	LSEAAMCYVHV
HC4	ATAQMKEHEKDPEMLIDLQYSLAKSYASTPELRKTWLD SMAKIHVKNGD	FSEAAMCYVHV
HC1	ATAQMKEHEKDPEMLVDLQYSLANSYASTPELRRTWLESMAKIHARNGD	LSEAAMCYIHI
HC3	DTVKMKEHQEDPEMLIDLMYRIAKGYQTS PDLRLTLWLQNMAGKHSERSN	HAEAAQCLVHS
HC5	DTVKMREFQEDPEMLMDLMYRIAKSYQAS PDLRLTLWLQNMAEKHTKKKC	YTEAAMCLVHA

		SH3	
HC2A	TALVAEYL	TRKGV-----	FRQGCTAFRVITPN
KIAA	TALVAEYL	TRKEA-----	VQWEPPLPHSHSACLRRSRGGVFRQGCTAFRVITPN
rat	TALVAEYL	TRKEAD-----	LALQREPPVFPYSHTSCQRKSRGGMFRQGCTAFRVITPN
HC4	AALVAEFL	HRKKL-----	FPNGCSAFKKITPN
HC1	AALIAEYL	KRKG YWKVEKIC	TASLLSEDT HPCDSNSLLTTFSGGSMFMSGWPAFLSITPN
HC3	AALVAEYL	SMLED-----	RKYL PVGCVTFQNISSN
HC5	AALVAEYL	SMLED-----	HSYLPVGSVSFQNISSN

FIG. 3A (3 of 5)

	PBM
HC2A	SSVV-----
KIAA	-----
rat	CVTLPEPHVGTCTCFVMCKLRITTFRANHWFCQAQEEAMGNGREKEPWTVIFNSRFYRSWGK
HC4	EV-----
HC1	SAEV-----
HC3	-----
HC5	-----

HC2A	-----
KIAA	-----
rat	VHIFF
HC4	-----
HC1	-----
HC3	-----
HC5	-----

FIG. 3A (5 of 5)

	A	B	
CLASP-1	YRVAFYGQ	Q:::GFFEEEGKEYIYKEP	
KIAA1058	FRVAFFGQ	AAQYQFTDSETDVEGFFEDEGKEYIYKEP	
CLASP-2		FEDEGKEYIYKEP	
CLASP-6	FRVAFFGQ	Q:::GFFEEDEGKEYIYKEP	
CLASP-4	FRVAFYGQ	Q:::SFFEEEDGKEYIYKEP	
DOCK180	FAVGYYGQ	Q:::GFPTFLRGKVFIYRGKEYERRED	
DOCK2	FAVGYYGQ	Q:::GFPSFLRNKVFIYRGKEYERRED	
DOCK3	FRVGFYGR	Q:::KFPFFLRNKEYVCRGH	
KIAA0716	FRVGFYGR	Q:::KFPFFLRNKEYVCRGH	
CLASP-3	FRVGFYGT	Q:::KFGDLDEQEFVYKEP	
CONSENSUS	F V FYG	KEY K	
	YF	Q F R	
			C
TRG	PKLTPLSEISQRLLKLYSDKFGSENVKMIQDSGKVNPKDLDSKFAY	YIQVTHVTPFFDEKE	
CLASP-1	PKLTGLSEISQRLLKLYADKFGADNVKIQDSNKNPNKDLDPKYAY	YIQVTYVTPFFEEKE	
CLASP-2	PKLTPLSEISQRLLKLYSDKFGSENVKMTQDSGKVNPKDLDSKYAY	YIQVTHVTPFFDEKE	
CLASP-4	PKLTGLSEISLRLLVLYGKFGTENVKIQDSKVNKELDPKYAH	YIQVTYVTPFFDKE	
CLASP-3	PAITKLAEISHRLEGFYGERFGEDVVEVIKDSNPVCKCLDPNKAY	YIQITYVEPYFDIYE	
KIAA0716	HDYERLEAFQQRMLNEFPFAIA-----MQHANQPDETIFQAEAC	YQLQIYAVTPIPEBQE	
DOCK3	HDYERLEAFQQRMLSEFPQAVA-----MQHPNHPDDAILQCDAC	YQLQIYAVTPIPDYVD	
DOCK2	FQMQLMTQFPNAEK-----MNTTSAPGDDVKNAPGC	YIQCFVQPVLDHP	
DOCK180	EYERREDFQMQLMTQFPNAEK-----MNTTSAPGDDVKNAPGC	YIQCFVQPVLDHP	
CONSENSUS	L L Y	YIQ+ V P D	
	M F	L E	
	D	E	
CLASP-1	RTIILTSHLFPYVKKRIQVISQSSTELNPIEVAIDEMSRKVSELN		
TRG	RTIILTAIHCFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVVELH		
KIAA1058	RTIILTAIHCFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVVELR		
CLASP-2	RTIILTAIHCFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVVELR		
CLASP-6	RTIILTAIHCFPYVKKRIPFMYQHHTDLNPIEV:HDEM	SKKVVELR	
CLASP-4	RTIILTTSNSFPYVKKRIPINCEQQINLKPIDVATDEIKDKTAELO		
CLASP-3	KTIIITTSHAFPIYKTRVNVTHKEEILTPIEVAIEDMQKKTQELA		
CLASP-5	NTVITTMHAFPIYKTRISVIQKEEFVLTPIEVAIEDMKKKTQLLA		
KIAA0716	RTSLYLVSPLPGISRWFVEVEKREVVEMSPLENAIEVLNKNQQLK		
DOCK2	RTSEVTAYKLPGLRWFEVVHMSQTTISPLENAIETMSTANEKIL		
DOCK3	RTTILTLTHSLPGISRWFEVERRELVEVSPLENAIQVVENKNQELR		
DOCK180	RTSEVTAYKLPGLRWFEVVHMSQTTISPLENAIETMSTANEKIL		
CONSENSUS	RT I FP V + V + P+E AI+ M +L		
	F L L	+	I

FIG. 3B (1 of 2)

	F										G									
CLASP-1	SLQLKLGSVSVKVNAGPMAYARAFLEETNAKKYEDNQV--KLLKEIFRQFADACGQALD																			
TRG	KLQLKLGSVSVQVNAGPLAYARAFLLDDTNTKRYEDNKV--KLLKEVFRQFVEACGQALA																			
KIAA1058	KLQLKLGSVSVQVNAGPLAYARAFLLDDTNTKRYEDNKV--KLLKEVFRQFVEACGQALA																			
CLASP-2	KLQLKLGSVSVQVNAGPLAYARAFLLDDTNTKRYEDNKV--KLLKEVFRQFVEACGQALA																			
CLASP-6	KLQLKLGSVSVQVNAGPLAYARAFLLDDTNTKRYEDNKV--KLLKEVFRQFVEACGQALA																			
CLASP-3	MLQMLQGSGVGTTVNQGPLEVAQVFLSE--IPSDKLFRRHNNKLRCLCFKDFTKRCEDALR																			
CLASP-4	QLQLKLGCVSVQVNAGPLAYARAFLLDSQASKYFPKKVSELKDMFRKFI--QACSI																			
CLASP-5	MLQMLQGSGVGTTVNQGPLEVAQVFLAE--IPADKLYRRHNNKLRCLCFKEFIMRCGEAVE																			
KIAA0716	PLTMCLNGVIDAAVNGGVSRYQEAFVKEYILSHEDGEKIARLRELMLEQAQILEFGLA																			
DOCK2	PLSMLLNGIVDPAVMGGFAKYEKAFTEEYVRDHPEDQDKLTHLKDLIAWQIPFLGAGIK																			
DOCK3	ILSMCLNGVIDAAVNGGIARYQEAFDDKYINKHFGDAEKITQLKELMQEQVHVLGVGLA																			
DOCK180	PLSMLLNGIVDPAVMGGFAKYEKAFTEEYVRDHPHAHEKIEKLKDLIAWQIPFLAEGIR																			
CONSENSUS	L	M	L+G	V	VN	G	Y	AFL	+	+	F							L+		L
				I			V	V	F	+										I

DOCK2=KIAA0209
DOCK3=KIAA0299
CLASP2variant=KIAA1058

FIG. 3B (2 of 2)

2 32
CGA GTA AAT CGT TCT CGA AGC CTT AGT AAT AGC AAT CCA GAT ATA TCT GGG ACT CCC ACG
62 92
TCA CCA GAT GAT GAA GTT CGA TCA ATC ATC GGG AGT AAG GGT TTA GAT CGC TCC AAT TCC
122 152
TGG GTT AAC ACT GGT GGT CCA AAA GCT GCC CCA TGG GGA TCC AAC CCC AGT CCA AGT GCA
182 212
GAA TCA ACA CAG GCT ATG GAT CGA AGT TGT AAT CGT ATG TCT TCG CAC ACA GAG ACG TCA
met asp arg ser cys asn arg met ser ser his thr glu thr ser
242 272
AGT TTC TTA CAA ACA TTA ACG GGA CGC TTA CCA ACT AAA AAG CTT TTT CAC GAG GAG CTG
ser phe leu gln thr leu thr gly arg leu pro thr lys lys leu phe his glu glu leu
302 332
GCT TTG CAG TGG GTT GTT TGC AGT GGC AGC GTT CGG GAA TCA GCT TTG CAA CAA GCC TGG
ala leu gln trp val val cys ser gly ser val arg glu ser ala leu gln gln ala trp
ref 1.1 and 1.2
362 ref 2.1 and 2.2 ↓ 392
TTC TTT TTT GAA TTA ATG GTA AAG AGC ATG GTG CAC CAT TTA TAC TTT AAT GAT AAA CTT
phe phe phe glu leu met val lys ser met val his his leu tyr phe asn asp lys leu
422 452
GAG GCT CCA AGG AAA AGT CGT TTT CCA GAA CGT TTC ATG GAT GAC ATT GCA GCT CTT GTC
glu ala pro arg lys ser arg phe pro glu arg phe met asp asp ile ala ala leu val
482 512
AGC ACG ATT GCT AGT GAT ATA GTT TCA CGA TTT CAG AAG GAC ACA GAA ATG GTT GAG AGA
ser thr ile ala ser asp ile val ser arg phe gln lys asp thr glu met val glu arg
542 572
CTC AAT ACA AGC CTT GCA TTC TTT CTC AAT GAT CTG TTG TCT GTT ATG GAC AGA GGA TTT
leu asn thr ser leu ala phe phe leu asn asp leu leu ser val met asp arg gly phe
602 632
GTT TTT AGC CTT ATA AAG TCC TGC TAT AAA CAG GTG TCT TCA AAG CTT TAC TCA TTA CCG
val phe ser leu ile lys ser cys tyr lys gln val ser ser lys leu tyr ser leu pro
ref 3.1 and 3.2
662 692
AAT CCC AGT GTT CTG GTG TCC TTG AGG CTG GAT TTT CTA CGA ATC ATC TGC AGT CAT GAG
asn pro ser val leu val ser leu arg leu asp phe leu arg ile ile cys ser his glu
722 752
CAC TAT GTT ACA TTA AAC TTA CCC TGC AGC TTA CTT ACT CCA CCT GCA TCT CCA TCA CCT
his tyr val thr leu asn leu pro cys ser leu leu thr pro pro ala ser pro ser pro
ref 4.1 and 4.2 ↓ 815
782 815
TCT GTT TCT TCT GCA ACA TCT CAG AGT TCT GGA TTT TCT ACG AAT GTA CAA GAC CAA AAG
ser val ser ser ala thr ser gln ser ser gly phe ser thr asn val gln asp gln lys
842 872
ATT GCA AAT ATG TTT GAA TTA TCC GTG CCT TTC CGC CAA CAG CAT TAT TTG GCA GGA CTT
ile ala asn met phe glu leu ser val pro phe arg gln gln his tyr leu ala gly leu

FIG. 4A (1 of 14)

902	GTG TTA ACA GAG CTG GCT GTC ATT TTA gac	932	cct gat gct gaa gga ctg TTT GGA TTG CAT
	val leu thr glu leu ala val ile leu asp		pro asp ala glu gly leu phe gly leu his
962	AAG AAA GTC ATC AAT ATG GTA CAC AAT TTA	992	CTC TCC AGT CAC GAC TCA GAC CCG CGG TAC
	lys lys val ile asn met val his asn leu		leu ser ser his asp ser asp pro arg tyr
1022	TCT GAC CCT CAG ATA AAG GCT CGA GTG GCC	1052	ATG TTG TAT CTA CCT CTG ATT GGT ATT ATC
	ser asp pro gln ile lys ala arg val ala		met leu tyr leu pro leu ile gly ile ile
1082	ATG GAA ACT GTA CCT CAG CTG TAT GAT TTT	1112	ACA GAA ACT CAC AAT CAA CGA GGA AGA CCA
	met glu thr val pro gln leu tyr asp phe		thr glu thr his asn gln arg gly arg pro
1142	ATT TGT ATA GCC ACT GAT GAT TAT GAA AGT	1172	GAG AGC GGA AGT ATG ATA AGC CAG ACC GTT
	ile cys ile ala thr asp asp tyr glu ser		glu ser gly ser met ile ser gln thr val
1202	GCC ATG GCA ATC GCA GGG ACA TCG GTC CCT	1232	CAA CTA ACA AGG CCT GGC AGT TTC CTC CTC
	ala met ala ile ala gly thr ser val pro		gln leu thr arg pro gly ser phe leu leu
	↓ ref5.1 and 5.2		
1262	ACG TCA ACG AGT GGC AGG CAA CAC ACT ACC	1292	TTT TCA GCA GAA TCA AGT CGA AGC CTT TTG
	thr ser thr ser gly arg gln his thr thr		phe ser ala glu ser ser arg ser leu leu
1322	ATC TGT CTA CTT TGG GTT CTC AAA AAT GCA	1352	GAT GAA ACA GTT CTA CAG AAG TGG TTT ACA
	ile cys leu leu trp val leu lys asn ala		asp glu thr val leu gln lys trp phe thr
1382	GAT CTC TCA GTC TTG CAG CTA AAC CGG CTA	1412	TTA GAT CTG CTT TAT CTC TGT GTG TCT TGC
	asp leu ser val leu gln leu asn arg leu		leu asp leu leu tyr leu cys val ser cys
1442	TTT GAG TAT AAA GGG AAA AAA GTG TTT GAA	1472	CGA ATG AAT AGC TTG ACC TTT AAG AAA TCA
	phe glu tyr lys gly lys lys val phe glu		arg met asn ser leu thr phe lys lys ser
1502	AAA GAC ATG AGA GCA AAG CTT GAA GAA GCT	1532	ATT CTT GGG AGC ATA GGT GCC AGG CAA GAA
	lys asp met arg ala lys leu glu glu		ala ile leu gly ser ile gly ala arg gln glu
	↓ ref 6.1 and 6.2		
1562	ATG GTA CGG CGA AGC CGA GGA CAG CTC GAG	1592	AGA AGC CCA TCT GGA AGT GCC TTT GGA AGT
	met val arg arg ser arg gly gln leu glu		arg ser pro ser gly ser ala phe gly ser
1622	CAA GAA AAT TTG AGG TGG AGG AAA GAT ATG	1652	ACT CAC TGG CGT CAA AAC ACA GAG AAG CTT
	gln glu asn leu arg trp arg lys asp met		thr his trp arg gln asn thr glu lys leu
1682	GAC AAA TCA AGA GCA GAG ATT GAA CAC GAA	1712	GCA CTG ATT GAT GGA AAC CTG GCT ACA GAA
	asp lys ser arg ala glu ile glu his glu		ala leu ile asp gly asn leu ala thr glu

FIG. 4A (2 of 14)

1742	1772
GCA AAC CTA ATC ATT TTA GAT ACA TTA GAG	ATT GTT GTT CAG ACC GTT TCT GTA ACG GAA
ala asn leu ile ile leu asp thr leu glu	ile val val gln thr val ser val thr glu
1802	1832
TCC AAA GAG AGC ATT CTT GGT GGA GTG CTA	AAA GTG CTA CTA CAC AGC ATG GCC TGT AAC
ser lys glu ser ile leu gly gly val leu	lys val leu leu his ser met ala cys asn
	ref 7.1 and 7.2 ↓
1862	1892
CAA AGT GCA GTT TAT CTA CAA CAC TGT TTT	GCT ACA CAG AGA GCC TTG GTT TCA AAG TTT
gln ser ala val tyr leu gln his cys phe	ala thr gln arg ala leu val ser lys phe
1922	1952
CCT GAA CTC TTA TTT GAA GAA GAG ACA GAG	CAG TGT GCT GAT TTA TGC CTC AGG CTT CTC
pro glu leu leu phe glu glu glu thr glu	gln cys ala asp leu cys leu arg leu leu
1982	2012
CGA CAC TGT AGC AGT AGC ATC GGT ACA ATA	CGG TCA CAC CCC AGT GCC TCC CTT TAC CTA
arg his cys ser ser ser ile gly thr ile	arg ser his pro ser ala ser leu tyr leu
2042	2072
CTA ATG AGG CAA AAC TTT GAG ATT GGG AAT	AAC TTT GCC AGG GTT AAA ATG CAG GTA CCA
leu met arg gln asn phe glu ile gly asn	asn phe ala arg val lys met gln val pro
2102	2132
ATG TCA CTA TCC TCC TTG GTG GGC ACA TCT	CAG AAT TTT AAT GAA GAA TTC TTA AGA CGT
met ser leu ser ser leu val gly thr ser	gln asn phe asn glu glu phe leu arg arg
2162	2192
TCT CTA AAG ACT ATA TTG ACA TAT GCT GAA	GAA GAT CTG GAA TTG AGG GAA ACA ACA TTT
ser leu lys thr ile leu thr tyr ala glu	glu asp leu glu leu arg glu thr thr phe
2222	2252
CCT GAT CAG GTC CAG GAT CTG GTT TTC AAT	CTC CAT ATG ATT CTT TCT GAT ACT GTG AAA
pro asp gln val gln asp leu val phe asn	leu his met ile leu ser asp thr val lys
2282	2312
ATG AAG GAA CAC CAG GAG GAT CCT GAA ATG	TTG ATT GAT CTA ATG tac aga att gcc aag
met lys glu his gln glu asp pro glu met	leu ile asp leu met tyr arg ile ala lys
2342	2372
ggt tac CAG ACC TCT CCA GAT CTG CGA TTG	ACC TGG TTG CAG AAC ATG GCA GGC AAG CAC
gly tyr gln thr ser pro asp leu arg leu	thr trp leu gln asn met ala gly lys his
2402	2432
TCA GAA CGA AGC AAT CAT GCT GAA GCT GCA	CAG TGT CTA GTC CAC TCA GCA GCA CTT GTT
ser glu arg ser asn his ala glu ala ala	gln cys leu val his ser ala ala leu val
2462	2492
GCT GAA TAT TTG AGC ATG CTG GAG GAC CGG	AAA TAT CTT CCT GTG GGA TGT GTA ACA TTT
ala glu tyr leu ser met leu glu asp arg	lys tyr leu pro val gly cys val thr phe
↓ ref 8.1 and 8.2	
2525	2552
CAG AAT ATT TCA TCT AAT GTT TTA GAA GAA	TCT GCG GTC TCA GAT GAT GTG GTA TCT CCA
gln asn ile ser ser asn val leu glu glu	ser ala val ser asp asp val val ser pro
2582	2612
GAT GAA GAA GGT ATC TGC TCT GGA AAA TAC	TTT ACT GAG TCA GGA CTT GTG GGA TTA CTG
asp glu glu gly ile cys ser gly lys tyr	phe thr glu ser gly leu val gly leu leu

FIG. 4A (3 of 14)

2642	2672
GAA CAA GCA GCT GCT TCC TTC TCT ATG GCT GGC ATG TAT GAA GCA GTT AAT GAA GTT TAC	
glu gln ala ala ala ser phe ser met ala gly met tyr glu ala val asn glu val tyr	
2702	2732
AAA GTA CTT ATT CCT ATT CAT GAA GCT AAT CGG GAT GCA AAG AAA CTA TCC ACA ATT CAT	
lys val leu ile pro ile his glu ala asn arg asp ala lys lys leu ser thr ile his	
	ref 9.1
2762	2792
GGT AAA CTT CAA GAA GCA TTC AGC AAA ATT GTT CAT CAG AGT ACT GGC TGG GAG CGG ATG	
gly lys leu gln glu ala phe ser lys ile val his gln ser thr gly trp glu arg met	
2822	2852
TTT GGC ACC TAT TTT CGT GTT GGT TTT TAT GGA ACC AAG TTC GGG GAT TTG GAT GAA CAA	
phe gly thr tyr phe arg val gly phe tyr gly thr lys phe gly asp leu asp glu gln	
2882	2912
GAA TTT GTT TAC AAG GAG CCT GCA ATA ACC AAA CTT GCA GAG ATA TCT CAC AGA TTG GAG	
glu phe val tyr lys glu pro ala ile thr lys leu ala glu ile ser his arg leu glu	
↓ ref 10.1 and 10.2	
2945	2972
GGA TTT TAC GGA GAA AGA TTT GGA GAG GAT GTG GTT GAA GTA ATC AAA GAC TCT AAT CCT	
gly phe tyr gly glu arg phe gly glu asp val val glu val ile lys asp ser asn pro	
3002	3032
GTA GAC AAG TGT AAA TTA GAT CCT AAC AAG GCA TAT ATT CAG ATT ACC TAT GTG GAG CCA	
val asp lys cys lys leu asp pro asn lys ala tyr ile gln ile thr tyr val glu pro	
3062	3092
TAC TTT GAC ACA TAT GAG ATG AAG GAC AGA ATC ACC TAT TTC GAC AAA AAT TAC AAT CTT	
tyr phe asp thr tyr glu met lys asp arg ile thr tyr phe asp lys asn tyr asn leu	
3122	3152
CGT CGA TTC ATG TAC TGT ACA CCC TTT ACT TTA GAT GGC CGT GCC CAT GGG GAA CTT CAT	
arg arg phe met tyr cys thr pro phe thr leu asp gly arg ala his gly glu leu his	
3182	3212
GAA CAA TTC AAA AGG AAG ACC ATT CTG ACT ACG TCT CAT GCC TTT CCT TAT ATT AAA ACA	
glu gln phe lys arg lys thr ile leu thr thr ser his ala phe pro tyr ile lys thr	
	ref 11.1
3242	3272
AGG GTC AAT GTC ACT CAT AAA GAA GAG ATC ATC TTA ACA CCA ATT GAA GTT GCT ATT GAG	
arg val asn val thr his lys glu glu ile ile leu thr pro ile glu val ala ile glu	
3302	3332
GAC ATG CAG AAA AAG ACA CAG GAG TTG GCA TTT GCA ACA CAT CAG GAT CCC GCA GAC CCC	
asp met gln lys lys thr gln glu leu ala phe ala thr his gln asp pro ala asp pro	
3362	3392
AAA ATG CTT CAG ATG GTA CTC CAG GGA TCT GTA GGC ACC ACA GTG AAT CAG GGG CCT TTG	
lys met leu gln met val leu gln gly ser val gly thr thr val asn gln gly pro leu	
3422	3452
GAA GTT GCC CAG GTT TTT CTG TCT GAA ATA CCT AGT GAC CCA AAG CTC TTC AGA CAT CAT	
glu val ala gln val phe leu ser glu ile pro ser asp pro lys leu phe arg his his	
3482	3512
AAT AAA CTG CGA CTC TGC TTT AAA GAT TTT ACT AAA AGG TGT GAA GAT GCC TTA AGA AAA	
asn lys leu arg leu cys phe lys asp phe thr lys arg cys glu asp ala leu arg lys	

FIG. 4A (4 of 14)

3542		3572
AAT AAG AGC TTA ATT GGG CCG GTT CAA AAG	GAG TAT CAA AGG GAA TTG GGG AAA CTA TCT	
asn lys ser leu ile gly pro val gln lys	glu tyr gln arg glu leu gly lys leu ser	
3602		3632
TCG CCT TAA AGA GGC CCT ACA GCC CTA GAT	CAC AGA AAG TCC CTC AGT TAT CCA AGC CAG	
ser pro OCH		
3662		3692
TAT TGC TTG TCC CCT GCC ACA GAG ATT CCT	TCA GTC GAA TGA GCT TTC GCA AAA TGG ATC	
3722		3752
TCT AAA CTG AAT GCA CTT GTT TTA TTC ATC	TGC AAA GAG CCA TGT ATT CAA CAT CGA GTG	
3782		3812
TGA AAA GAT CTA TTG GAA ACC AAC ATG GAA	TGG AAT TCT GGA AAT TAT TAT TCA TTG AAG	
3842		3872
AAT GCA GTG GCC AAG AAA ATA TCA AAT GTA	GAT TGT TAA CGC TTG AGA ATC ATG GCT ATG	
3902		3932
GTT TCT AAT GTT CGG GTA ACA AGC TGT TAT	CTT TTA AGA CAT TTT AAT GAC TCA AAG GTA	
3962		3992
CAC TAT ACA TTT ACC ATT ATT TAT ACC ATA	GCT AAG GTT AAA AAT TTA TTC ACT TTA AGT	
4022		4052
TCG TAT TTT TTA ATT TAT ATC ACC ATT TAT	AGA TTC ATT TTG GAC CCA TTT TAA ATG TAG	
4082		4112
TAA TGC TTA TTT TAA AGG TAC TAA AAA ATA	TGT GAA TGT TTA CCT CGT GCG CGC CAG GGC	
4142		
CTC		



ref 12.1

FIG. 4A (5 of 14)

Ref 1.1

Sequence of BAC8 using primer C3S3, which spans nucleotides 341-360 of the cDNA. Exon sequence is underlined and represents nucleotides 365-381.

TTTTTTGAATTAATGGTGAGCAAAACTGAGCATGTTCTTTAATATTTTTCTCTTAGTG
AACAATTTTATGCTAGCTCATTTGTTACCTTAGAAATCTTTTTCTGTTGCACATCTTAAC
GCTTTTCCATGTGCCTCTAAGACAAAATTACATGTGTTACATCTCTAAATAAACACTGT
GGACACTCAACACAGTTTAGGTGGAATTAAGAGTGAGGCTCATTTTAACTCTTATTTTC
TCAGGGATGGTTGCATAAGCTAGCTATATTTTCAAAGGAACTTGTGATACATTCTTTG
CTAGTCATTATACATGAAGTGTATAATGACAGTATTGTAGATTTTATACCAAAGATGG
AAAGAGCTTTATAGATACCCACTGCTATTGTTATGGCTAGTAAACCCTTAGGGAAATG
CCAGTTACAATCAATAAAAAACAACAGTCTGGCTGGGTGCAGTGGCTCACACCTGTA
ATCTCAGCACTTTAGAAGGCCGAGGCAGGAGGATC ACTTGAGATCAGGAGTTTGAGAC
CCAGCCTGGGCAACATAGCAAGAGCCCATATNTACCCAAAAAAAATTTTTTTTTTAAAT
TAAGCTAAAACCCTGGNNGGCCACAAAACCTGTAGTTCCCATCTACTTTGGAAAGGCT
TGAAGGANGGGAGGGCTTGCTTTGAGCCCCAAGAANGTTCAAAGGCTNGCNGNCAGG
TTNTGATTCNACACNTGCAACTCCCGCATTGGGTNAACAAAANCCAAGGAANC.

Ref 1.2

Sequence of BAC9 using primer C3S3, which spans nucleotides 341-360 of the cDNA. Exon sequence is underlined and represents nucleotides 372-381.

AATTAATGGTGAGCAAAACTGAGCATGTTCTTTAATATTTTTCTCTTAGTGAACAAT
TTTATGCTAGCTCATTTGTTACCTTAGAAATCTTTTTCTGTTGCACATCTTAACGCTTTT
CCATGTGCCTCTAAGACAAAATTACATGTGTTACATCTCTAAATAAACACTGTGGACA
CTCAACACAGTTTAGGTGGAATTAAGAGTGAGGCTCATTTTAACTCTTATTTTCTCAGG
GATGGTTGCATAAGCTAGCTATATTTTCAAAGGAACTTGTGATACATTCTTTGCTAGT
CATTATACATGAAGTGTATAATGACAGTATTGTAGATTTTATACCAAAGATGGAAAGA
GCTTTATAGATACCCACTGCTATTGTTNTGGCTAGTAAACCCTTANGGAAATGCCAGTT
NCAATCAATAAAAAACAACAGTACTGGCTGGGTGCAGTGGCTTACACCTGTAATCTC
AGCACTTTATAAGGCCCNAGGCNGGAGGATCACTTNAGATCCAGGAGTTTGAGACCAG
CCTGGGCAACATANCAAGAGCCCATTATCTACCAAAAAANTTTTTTTTTTAAATTAAG
CTAAACNCTGGGTGGNACAAACCTGTTNGNTTCNATNTNCCTTTGGAAAAGCTTANG
AAGGGGAGGGCTTNCCTTTGGANCCCCAAGTTNAAAGGGNTTGCAGTCAGCCTTTT
NAATCACCCNNGGNCCTNTCGCATTGGGATTNCCAANANGCCAANGNAACCCCGNT
CNTNTTTTTAAAAAANTNTTTTTAAAGNANNTTTNTTNGN

Ref 2.1

Sequence of BAC8 using primer HC3AS7, which spans nucleotides 387-406 of the cDNA. Exon sequence is underlined and represents nucleotides 382-386.

TCTTTNNGAAAAAGATTANATTATTAATTCTATGATATATTAAACAATACACANCTCTAA
CACTTGGAATAATTTTAAATATGGCATGTAATTTAATAGATGACTGAAATATTTTAGC
TTCTCAAATATTTTTTAAAGTTCCTACAAATGTTTTGTATTTGCTTAAAATAAAATANA
AAAACCACCATATTACTTTTCAGAAAATTATGCTAGCTAACAATAGGACAAAAAATTCT
GTGTATGTCAACAAAAAAATTCACCTTAAATTTTTTTTTTTCCATAAAAAACAGGGC
TACTTGCCAGGTGAGANGTGCTGCCGTATGAGCTCCTCGNTAGATTGCGCNGCCGGA
NTGTCGGNCCCTNCGTTTAAATATAACGGCGTGNGCNTGTACCGCAGGCTNTGCTAGGT
CGTGNTCCCAAGATATCNTNTNTANCATANTAGACGNTGGNGNCGNNTGCATGTGGCN
TNATTNTNGCAATTGTNACAATCCTAGTNTGTACNTNANAGNTCNGCCNCTGTGANNT
CGTTGTATAGTCNGNGGCNCGCTTGNTTCTGATGCTGAGAGCANTNNCNNACTNTTNN
NCNCCCATCTTNCNNTTNNNNNCCCCNTTTNNATNNNTTTNNNTNNCNNNNNNATNT
NTNAANNNAACCNCC

Ref 2.2

Sequence of BAC9 using primer HC3AS7, which spans nucleotides 387-406 of the cDNA. Exon sequence is not found within this sequence. Since the primer is directed against exon sequence we presume that sequence derived from HC3AS7 is intron sequence. Additionally, this sequence matches the intron sequence found in the previous sequence (BAC8 sequenced with HC3AS7).

GCGCTNCCNNNTNNTTTATCTTCTGAAAAGACTNATATNATTCTATGATTATAACATTA
CACACTCTAACACTGGACTTNTTAAATATGGATGTAATTAATAGATGACTGAATATTTT
AGCTTCTCAAATATNTTTAANGTCCCTACAATGTTTGNATNTGCTTAAAATAAAATANA
AAACCCCATATTACTTTTCAGAAAANTATGCTAGCTAACCAATAGGACANAAAAATTCTG
TGTATGCAACAAAAAAATTCAACCTTNAATCTTCTTTTTTTTCCAATANAAAACAGGG
CTACTCTGCCACAGGCTGGAGTCAGTGGCTGATACAGCTACTGCAGCTCACTCCGGG
CTATGTGATTGCCTGCCTAAGCCTCNGAGTAGTAGGCTCAGGTGCCACTACATGCCAG
TAATCTAAAATTTATAGAGACAGGGCTGCTGTGTGNCCAGGCTGGCTAACTCCGGGCT
AAGCGTTCTTGCCCTNGCTCTAAATGTGGGATACAGNATGTATCATNCATCAGCCAAAA
AGTTAATTAANTTCCAGATNANTATTTGCATCAAAGCTCCAATNTAGCTTGAAGTAGA
ACCTGCTCNTTGGCTAGANTATCCCGNNTGTTATGGATCATATTANGCNNTTGTGATGC
CGAATGGNATCTATTCCGGGAGACANATTACTATNGGATGANAGCANATNGCCNNAT
GCTTNTTTGTAAACGCTNNANNTAAGAACNTTCTNGACATCGTCATAGNTCGAAGTNNT
NNGCGAANTTGATACTAANTTCATGNTANGCCNATGACTNTNGTGATTNNNTGANTGNCT
GGGAGAACCTACNTNCCCCNTACNNATANNCTNCACCCCTACTACTNTNCCNNTCNC
TCTCTANTTCTACTCCACNTTATTATCCTCNCCTTCNCATCNTCCCATCNTNATTCNAC
GCCNCNANACTTANCNTTNATNCACTCTNNCT

Ref 3.1

Sequence of BAC8 using primer C3AS4, which spans nucleotides 737-756 of the cDNA. Exon sequence is underlined and represents nucleotides 677-736.

TAATGTACATAGTGCTCATGACTGCAGATGATTTCGTAGAAAATCCAGCCTCAAGGACA
CCAGAACACTGGGATTCGGTAATGAGTAAAGCTTTGAAGACACCTTGTAAGCAATGCA
TAAGTAAGAGAACACCAATTGAATCTATTATTTCTTTAATACTAATACCAGAATGGCA
AATTAGAATTAAAGAGATAGTACTTGGTATCCAGTTTGGGTTTTGTGGCTTAAAGTAGCA
GTATCACCTTTTTCCAGAGTTACTGCTAAAATTAAAAATTTTAACTATCAGGTTTACT
GTATAAACATATTTGACTAACCTAAAAGCCACATTCTTGTATTTCCAATATAGCATCAA
TATTTCTACTTCTCATAAAACAGGGAAAACGTATATCACCAAAAATAACTTCTTATTAC
TTCCTTCTTAAAAGAAATTATCAATTCTTTTTATAGCACTTGTGCTTACCTGTATTTAT
AATTTGTCTGTTTTCTCAGCAACATCATAAGCTACTTGAGGAGACATACTATAAACTGA
TTTAACAGCTTTAGTGTCCCTACAGCTTAGCTCAATGTTTGACAAATATAGGAGATCAA
TGCTTAAAGGAATAAAGGCCAGGACAAGTTCTGGTAGCAAATAGTCCATAAAAGGTTT
TGGGGGAAAAGGGTAAAAATGGATACATATCGGGGTNGCAAGNTTTTTCCATGTGGGG
TGAGGTGCCCCATGCCTT

Ref 3.2

Sequence of BAC9 using primer C3AS4, which spans nucleotides 737-756 of the cDNA. Exon sequence is underlined and represents nucleotides 677-731.

TAACATAGTGCTCTGACTGCAGATGATTTCGTAGAAAAATCCAGCCTCAAGGACACCAGA
ACACTGGGATTTCGGTAATGAGTAAAGCTTTGAAGACACCTTGTAAGCAATGCATAAGT
AAGAGAACACCAATTGAATCTATTATTTCTTTAATACTAATACCAGAATGGCAAATTA
GAATTAAAGAGATAGTACTTGGTATCCAGTTTGGGTTTTGTGGCTTAAGTAGCAGTATC
ACCTTTTTCCAGAGTTACTGCTAAAAATTAAAAATTTAAACTATCAGGTTTACTGTATA
AACATATTTGACTAACCTAAAAGCCACATTCTTGATTTCCAATATAGCATCAATATTT
CTACTTCTCATAAAACAGGGAAAACGTATNTCACCAAAAATAAATTCTTATTACTTCCT
TCTTAAAAAGAAATTATCAATTCTTTTTATAGCACTTTGTGCTTACCCTGNATTTATAAT
TTGNCTGNTTTTCTCAGCAAACATCATAAGCTACTTGAGGGAGACATACTATTAAACCT
GATTACAGCTTTTANGTGTCCCTACAGCTTAACTCAATGTTTTGCAAAATNTNNGGAGA
TCAATGGCTTTAAAGAATAAAAGANCAGGGACAAGTTNTGGGTNGCCATNAGNACAA
TAAAGGTTTTNNGGGGAAAAGGGAAAAAATNGATTNCATNTCGNGGTTNGCAAGGTN
TTTTCCATTGNGGGGNGGAGGGGCCCATGCCATAANTTTAACCTTTCTTTTTTNGAAG
AAATTAAACNNTTAAAGGGGTN

Ref 4.1

Sequence of BAC8 using primer HC3AS6, which spans nucleotides 925-945 of the cDNA. Exon sequence is underlined and represents nucleotides 813-920.

CCAGTCTGCAATATGCTGTGCGAAGCCGATATCAACTTTGCATCTTTGTCTTGNCATTC
GAGAAATCAGACTTGTGGAAGTAGGAGACAGCTTACAGCGTGACAAGCTCTCAGCA
GAGCATATACGAATGAATCTTTTCCAGGGAGTTATTTATATACTACCTGAGCAAGCCA
CTTTAGCTTTGGGCAGGAACCTTNTGGATGTTATAAGTAATACTTATATGAATAATATGA
AATTAATATTTACTTCTTTTACANTCTTCTCTTTTCTTATCTTAGCCTTTATCCCCTTGT
GGAAAAGACACTATCAATGCTAGATNCTCCCAAGNCAGAGAATTATGCAGGTTTGGTC
AGAGAATCGACACAGACATGTTTACAGATTCTTCTTGAAATACATATTGTGCACGAGT
TTTTTACANTATCTCAATTTAGATCTCAGACAGCATNTNGACTAGNGGGTCTAGGACAT
AGATACATNTTTGNGAACTTCTATAGAANAACNTNTGCNTTAAAAAGGAGCTTGTNTG
ANANGAATNNNCTGNGAAGGGCCCGATACGANAATTTGACTTCGGNGAAAATTNNNG
GATTNNTACAAANTTCTAGGNGGCACCTTNAAAANGNNTGGGNACNTTGGNGGCGGA
AAAAAGCCCTTCNTTTAGNTNTCCNGAAATGGAAAAGTNCCAANTTCCNAAAAAA
ANGGGCTTTGTTNNCTTNCNANA

Ref 4.2

Sequence of BAC9 using primer HC3AS6, which spans nucleotides 929-949 of the cDNA. Exon sequence is underlined and represents nucleotides 813-924.

GACGCCAGCTCTGTACACAGTCTGCAATATGCTGTGCGGAAGGCCGATATCAACTATT
GCATCTTTGTCTNGNCATCGAGAAATCAGACTCTGTGGAAGNAGGCAGACAAGACTAT
ACAGCNTGCACANAGCATCTCAGCAGGCATATAAGAATGAANCTTTTCCAGGGAGTTA
TTTATATACTACCTGAGCAAGNACTTCAACTTNGGCAGGAACCTGTGGATGNTTATAA
GTATACTTATATGAATAANATNGAAATTAATATTTAATTCTTTTACTTCTTCTTTTCC
TTATCTTAGCCTTTATCCCCTCGTGAAAAAGAGCACTAATCAATGCTATTNCTNCCAAG
NCAGGAATTTATAGCAGGTTGGTCGAGAATCGACACGACATGTTTACAGANTCATCTT
GAATACATNATTGTGCACGAGTNTTTTACTCTATCTCAAAATATAGATCTCAGATCGTC
TATNGANTATGNGGTTCTAGGACATGATTACATTTTTNNGGAACTTCCATAGATAAAA
CNTNTACCTNAAAAANANGAGCCTGTTNGAAATNGAATCTACTNCTAAAGGGCNAGTNC
CANATTTTACTTCCGCGANATNTCNGGATGTTACAAGTCTAGGGGNCCTTTAGNACGT
TNGATNTTTGANCGGAAAAAGCCCTTCTANNGGTCNCCTAATGGAAGCGCCAATTCC
NAANAAGGNCTGTGTTNTTNGACATTTACCNNGNCCNTTTCTAATCAAACNTNCTCTTC
TNNNANCCNCANNCNNNCCTATANNCTATCNCTCNCNTNNNCTCNTCACTCTCNNC
NCTNTCTTCCNTTCTNCACTNTNNNNCTCCTNNNATNNNCTTCTCCNATCCNTCTCANN
NNNTCANNCTCCCTACNNTNCNCNTNTTACCATCTNCNCCNNCT

Ref 5.1

Sequence of BAC8 using primer C3S6, which spans nucleotides 1128-1147 of the cDNA. Exon sequence is underlined and represents nucleotides 1182-1270.

GTATGATCCGCCAGACCGCTGCCATGGCAATNGTAGGGACATCGGTCCCTCAACTAACAAG
GCCTGGCAGTTTCCTNCTCACGTCAACGGTCAAAACAATCCTTCTACAGAATTTTTTTTTC
TNGAAAGACAAATATTTACTAGGATATGCCCTTAAATATATGAGATGATTGTATCAGCTGA
TGCAAAAGTGCTCAGTTTTATTTATGAAAATATTAAAGTTCCAGAAATTAAACTGTCTTC
TCCCAAACAGTTTTTAAAAAATGATTACCTCAAGGTTTATGGGAAAAAGCCCCGATTCTGC
ATTCAGAATTTGGAAAAATTGCCTCATTATAGATAGCCATNTCTTTTTTTTTNTTTTTTTTAT
NCTTCAAGTCTTAGGGNACATGTGCACAACATGCAGGNTAGTTACATATGTATACATGTGC
CATGTTGGTGTGTGTCACCCANNAACCCGCAATTTAAACATTAGGTNTATCTCCAAATGCTA
TCCNTTACCCCTTCCCCCATNCCACAACAAGGCCCGGCNTTTNGATGTTCCCTTCTCTG
TGCCACTGTGTNTCACATTNCCNCTTCCNCCCTTANTNNNGTGCAGAACNTNGCCNGTN
GCCCTNTNTTTTTTNCCC

Ref 5.2

Sequence of BAC9 using primer C3S6, which spans nucleotides 1128-1147 of the cDNA. Exon sequence is underlined and represents nucleotides 1152-1270.

CCNCTGATGATTATGAAAGTGAGAGCGGAAGTATGATAAGCCAGACCGTTGCCATGGCAAT
CGCAGGGACATCGGTCCCTCAACTAACAAGGCCTGGCAGTTTCCTCCTCACGTCAACGGTA
AAACAATCCTCCTACAGAATTTTTTTTTTCTAGAAAGACAAATATTTACTAGGATATGCCC
TTAAATATATGAGATGATTGTATCAGCTTGATGCAAAAAGTGCTCAGGTTTATTTATGAAA
ATATTAAAGTTCAGAAATATTTAACTGTCTTCTCCCAACAGTTTTTAAAAAATGATACCTCA
GGTTTATGGGAAAAAAGCCCCGTATTCTGTCAATTCAGAAATTTGGAAAATTTGNCTCATT
ATAGATAGTTCATTTTCTTTTTTTTTTTTTTTTTTATACNTTTAAGTTTTTAAGGGGNAC
CATGTTGCACCAANATTGCAGGGGTTNGGTTACCATATGGTTATTNCCATTGGTNCCCC
CANTGTTTGGGGNGTTGGCTTTGCCACCCCGAGNGTAAACCNCCGNTGCGAATTTTTTA
AAACAANTTTTGGGGGTTATTANTNTNTTCCCAAAAATNGGCNTTTTTNCCCTTTNCCCCC
CTTTCNCCCNCCCNNTTCCCAACNNANCAAGGGGCCCCCGGTANTGGGGGAATAGNTTT
CCCCCCTTNCCCTNGNNGGGCCAATTGTGGGGNNNCTCCATTTGGNNTGCAAANTTCCCC
CACCCNTNATTGTTGGTGGNGAAACCATTTCCCGGGGGTTTGGGGGTTTTTTTTTGGTCCC
CNTTGCCCAANTAATTTTTGCNTTGAANAAAAAGAATGGGGTTTTTCCAAAGCTTTTNGTCN
CCATTTGNTCCCTTTANGGNCCNTTNGTTCNCCTTNCCANAANGGGCCAATGTGAAACNN
CCTTTCATTTTTTTTTTATTGGGGNTTNCNTTATGGN

Ref 6.1

Sequence of BAC8 using primer C3S7, which spans nucleotides 1514-1533 of the cDNA. Exon sequence is underlined and represents nucleotides 1536-1589.

TTCTTGGGAGCATAGGTGCCAGGCAAGAAATGGTACGGCGAAGCCGAGGACAGCTCGGTAC
GTACACAATAGCTTCTCCTCCTGGTGAGAATTTCTTCAATTCCTTGAGTTGTATATTGTA
ATGATCATTTGCTAGTCTTCAATGTCAATCCTATGCTTTTTAAAAAGTGTTTAAAGTGT
AACTGTGAATTAACCTGAATAATCATTTCTCTGCAGTAATAAAAGTTAGAATTCGTATTA
GGTGAGTCAGCATACCGCCCCCCCCCGTTTTCTCTAGAAAGTCTTCTCTAGAAAACGTT
CTCTAGAAAGTCCTATCTAGAAAACCTTCTCTAGAAAGTCCTTATGTGATTAATAGCATCC
ATCCTCCCTTTTTAAATAGACTTTATTTTTGTAGAGCAGTTTTAAGTTCACAGCAAAAGTG
AGCAATGGGTACAGAGATTTCCCATATACCCCTTAGTATGCGTAGCCTCCCCCATTATTAAC
ATCCCCCATCAAGAGTAGTGCAATTTGTTGTAACCTGGTGAACCTACATTAACACATCATCAC
CCAGAGTCCGCAGTTTACATTAGGGATCATTATATAACATCTATTTTTACTTTTTTTTTT
TTAGTTGAGACAAGATTCTCGCTCTGTACCCAAGCTGGAGTGCAGTCCNGTGGATTGTN
GGCTTACTGN

Ref 6.2

Sequence of BAC9 using primer C3S7, which spans nucleotides 1514-1533 of the cDNA. Exon sequence is underlined and represents nucleotides 1536-1589.

GTGCCGGCAAGAAATGGTACGGCGAAGCCGAGGACAGCTCGGTACGTACACAATAGCTT
CTCCTCCTGGTGAGAATTTCTTCAATTTCTTGTAGTTGTATATTGTAATGATCATTGTT
GCTAGTCTTCAATGTCAATCCTATGCTTTTTTAAAAAGTGTTTAAAGTGTAAGTACGNGAAT
TAACTTGAATAATCATTTCTCTGCAGTAATAAAAGTTAGAATCTGATTTAGGTGAGTC
AGCATACCGCCCCCCCCCGTTTTCTCTAGAAAGTCTTCTCTAGAAAACGTTCTCTAG
AAAGTCCTCTCTAGAAAACCTTTCTCTAGAAAGTCCTTATGTGATTAATAGCATCCATCC
TCCCTTTTTTAAATAAGACTTTATTTTTGTAGAGCAGTTTAAAGTTCACAGCAAAAGTGA
GCAAAGGGCAGAGATTTCCCATATACCCCTTAGTATGCGTAGCCTCCCCCATTATTAAC
ATCCCCATCAGAGTAAGNGCATTGTGTGTAAGTGGNGAACACATAATTNACCATTTNTN
ACCCACAGTCCCGCAGGTTTACATTTATGGGATCATTCCCCCTANTAAACCATTTTNT
TTACTTTTTTTTTTTTTTTAGGTTGAGACAAGAATTTTCGGCTTCTTGTGTACCCCCAAA
CTNGGTAGTAGNCNNACCGTCGNGNAATTTNTGGGGTTTCNTNGNGNNCANTTTGTGCN
NTCNNCTTNNCNCNAAGAANTTTTTTTTCCACCTTTTTTTTTCCCCCNAANANANNAN
CCTTCCCCCTTGGNGGANGCTGGGGACTTCNCAGNGGNGG

Ref 7.1

Sequence of BAC8 using primer C3S8, which spans nucleotides 1843-1861 of the cDNA. Exon sequence is underlined and represents nucleotides 1862-1918.

CAAAGTGCAGTTTATCTCAACACTGTTTTGCTCACAGAGAGCCTTGGTTTTCAAAGGTAG
GTTATTTTTGTACCTGCAGTGTTGTGACACTTTGTTTTTTTTTATTAACATTGTCTAAGAT
CATTTGACACATTTCATTGGTTAATATATGTAGTAATATATTAATGAATATGTGTAGTTA
AAATTTAAATAATAACCTAAGACCCTTAATTCTTCTTGCCTCTCTACTGCTGCCTGCC
TTTTAGAAATTTTTCATTTATTTCGAATCACCTTTAACCAGTTCTGGTTTGAAAAACAGTA
ACTTGGATGTGGAGAAGGGCCTGAAATTAATAGCCAATCTTAAATATGGGGCTTCTCTT
GTTTTCTCTTCACTTGGTTCTGTTTTTATAAAAACTCAATTTATAAAGAATTCAATAT
ATAAGCAATTCAACCCACTGAAATTATTTTATGATGAATGGAAAAGAAGGTATGTGTTT
GTTCAACTGCTTTAAATGTTTACTTCTTATATTTGTTTTCCCTTAGAAATATGTATATT
CTTAAATTTTGAAGGTAGCTATTTTCATTTTAAATCATCCTAGAGGATGGAATGCANAGAT
GTTGGATGAAAATAACTTACGTATTATTTTGTAAATAAATATAAGAATTCATATATGGTT
GATTACCTAAGTGTTTTATGCACATTCTGATAGAAAGCTTCACCAACAATCCCTTGNT
NGATATATTATTT

Ref 7.2

Sequence of BAC9 using primer C3S8, which spans nucleotides 1843-1861 of the cDNA. Exon sequence is underlined and represents nucleotides 1865-1918.

AAGTCAGTTTATCTACAACACTGTTTTGCTACACAGAGAGCCTTGGTTTTCAAAGGTAGG
TTATTTTGTACCTGCAGTGTTGTGACACTTTGTTTTTTTTTATTAACATTGTCTAAGATC
ATTTGACACATTTCATTGGTTAATATATGTAGTAATATATTAATGAATATGTGTAGTTAA
AATTTAAATAATAACCTAAGACCCTTAATTCTTCTTGCCTCTCTACTGCTGCCTGCCT
TTTAGAATTTTTTCATTTATTTCGAATCACCTTTAACCAGTTCTGGTTTGAAAAACAGTAA
CTTGGATGTGGAGAAGGGCCTGAAATTAATAGCCAATCTTAAATATGGGGCTTCTCTTG
NTTCTCTTCACTTGGTTCTGTTTTTATAAAAACTCAATTTATAAAGAATTCAATATA
TAAGCCATTACCCACTGAAATTATTTTATGATGAATGGAAAAGAAAGGTATGTGTTTG
TTCACCTGCTTTAAATGNGACNTCNAATATTTTGGNTTCCCTTAAGAAAATATGT
ATAATCCTTAAANTTTNGAAAGGGANGCTANTTTCATTTTTTNAATCAATCCTAANAG
GGATTGGGAAATGCNCAAGATTTTTTGATTGAAAAANAACCTTANCGNATTTAATTTTT
NGGNAATAAAATAATTAGNAATCCNTATTATGNTTNGAATTACCTAAAGTGGTTTTTA
TTGCCCCATTTTNTTGATATGNAAAGCCTTTACCAACCAAATCCCCNTTGNNAGGAA
TATTATTTTTTNANGGGCCTCNTNTTTGTGGGGNTGGAAGNAAAAACCTTTGTTCCAA
GGTCCCCNC

Ref 8.1

Sequence of BAC8 using primer C3S10, which spans nucleotides 2413-2432 of the cDNA. Exon sequence is underlined and represents nucleotides 2433-2524.

AGTGCTAGTCCTCAGCAGCACTTGTTGCTGAATATTTGAGCATGCTGGAGGACCGGAAA
TATCTTCCTGTGGGATGTGTAACATTTTCAGGTAGGAATCTTCCAGATGTACATTAAATC
AAGGTATATCTTTTTTTGGTTTTAGCTTTTCTCACTGGTGTTTAGATTTTTTTTAGTTTA
TAAGGAAAGCTTAAAGACTTAAGCCAATGCTTCACAAGGTGAATTAACATTTTCACAGTG
ATTGTCATTAATACATTTTTTAAGGAGTACTTCTTGTTGATTCTCTTTCCACAGTTTCTT
ACCTCTGAATTATCAGCACTATGCTTATTTATTCTCTTTGGCTTTACTGNCCTGNAATC
CCGTTACATACTTTAACATCTATGGAAATGTATTACTGATAATCAGAATTCAGTAGAAA
TTCTTAATTGGCTTTTACTTCACATAGCAGATATACCAACATTCTCTATTCCCTACATA
AAATATTAAGATTATTTTATGACTAATACCCATGACTCACAGATGAGTTTGCCCTCTAG
TAGGGTCATAATTCTGACCCACTAGTTGAATTCTCTGCTTACCAAGAGNCAGGTATGCT
TGCTTTTTCTTCAAAACCTGTTAAATAGTAGNNTTGGGGATATTNTAAAAATTAGGTAA
ATGGTATATCTTCTGGTGGAANCAAGAN

Ref 8.2

Sequence of BAC9 using primer C3S10, which spans nucleotides 2413-2432 of the cDNA. Exon sequence is underlined and represents nucleotides 2445-2524.

CAGCAGCACTTGTTGCTGAATATTTGAGCATGCTGGAGGACCGGAAATATCTTCCTGTG
GGATGTGTAACATTTTCAGGTAGGAATCTTCCAGATGTACATTAAATCAAGGTATATCTT
TTTTTGGTTTTTAGCTTTTCTCACTGGTGTTTAGATTTTTTTTAGTTTATAAGGAAAGCTT
AAAGACTTAAGCCAATGCTTCACAAGGTGAATTAACATTTTCACAGTGATTGTCATTAAT
ACATTTTTTAAGGAGTACTTCTTGTTGATTCTCTTTCCACAGTTTCTTACCTCTGAATTA
TCAGCACTATGCTTATTTATTCTCTTTGTCTTTACTGCCTTGTAATCCGTTACATACTT
TAACATCTATGGAAATGTATTACTGATAATCAGAATTCAGTAGAAATTCTTAATTGGCT
TNTTACTTCACATAGCAGATNTACCAACATTCTCTATTCCCTACATAAAATATTAGGAT
TATTTTATGACTAATAACCATGACTCACAGATTGAGTTTGCCCTCTANTAGGGTNCATAA
TTTCTGACCCACTAGTTGAATTCTCTGCTTACCAAAAAGTCANTTATGCCTTTGCTTTTT
CTTCAAAACCTGNTTAATTAGGNACGGCTTTGGAGATAATTTATAAAAAATTTCAAGC
TNAANTGGNTTATTATTCTNTCCNNGGTTGAAAAAACCCAGGAATTGGCACAAANNAA
NAAAAAGNTTATTCCNNGGTTCTTTNCGGNAAAAAACCAAAAAATCTTNGAAATTGTT
TTTTACCAAAAANGACCTCCNCGGGAAAAAGGGNGTAAATTTNTTCCNTAAAAACNN

Ref 9.1

Sequence of BAC9 using primer C3S11, which spans nucleotides 2680-2699 of the cDNA. Exon sequence is underlined and represents nucleotides 2712-2800.

TTCCTATTCATGAAGCTAATCGGGATGCAAAGAACTATCCACAATTCATGGTAAACTT
CAAGAAGCATTTCAGCAAAATTGTTTCATCAGGTAATGATTCCAATTTCTAGCTTCACTAT
AAAGGGAAAAAACTGTCTGAAAGCATTAAATGTTGTTTTGCACTGATGTCAAACCTAGATC
CCGTGAAATGACCATTTTAATCAGACTACAAATGAGCGGTCAAAATGATAGTTCATGGC
CAAAGCAAAGCTCATTAACAATAAAAATGAATTCACCTAAAGTAAATGGTGATCATCAT
AAACTTTCTGCATAGCTTTTTTTTTTTTCATTTTTGAATTATTAATTAAGCAAGTTTTTA
AAAATTGTGATTTTTCTGTTTCACAAGGNAAGATCATAAGTTGNGGAATCTCATTTTTTA
AAATTGATACCCATATTNCTTTTGGCTGNGGAAAAANTGGAAGTTTTTTAATATTTTCAAGG
TTTTTTTTTAAATTTNAAATGGATTGTGGAAAACCTTTTAAATNAATTTAAACCTACCT
AAAATANTTTTTTTAATGGNCCNNGCCANCTGGAACNTTTTATTTTTTTCCCTAGGA
ATGGTTTTTACCCAAATCCATTCCCTTTTGAATAATATTTTTCCCTNAATTNCCAAAAA
ANTTTTTNTTTTTTTGGGNGGAAAAAATANTTGGAAAATTAAAAAATGGGGGTGGGGC
CNTAAATGGGGATTATTTTTAAATTTCTTAAAAAAGGGANTTTTCCATTTACCTTTNAA
TCCTTTTTTGGGNGGNTTCNATTTATTGGGGAATCCTNCNCTTTTTNTNCNCCTTAAAA
AANTTAGGGCCTNCCAAAATTTTAAACNNTTTAATTTTTNAAAANGGAAAGGNCCCCCT
TTCTTNGCCCGGTTGGTTT

Ref 10.1

Sequence of BAC8 using primer C3S12, which spans nucleotides 2909-2928 of the cDNA. Exon sequence is underlined and represents nucleotides 2929-2942.

TACAGATTGGAGGTGAATGCTGTGGTGGTTCATAAAATGTCATCTTTAGTTTGTATTCT
CTCTGATGATTAGACTTTCAGATCCAGATCTAATCATTTAGTAAGCCAGATCTTGCCAA
ATAAACTACTCCGTTAGAGAATAAGGACTTTTAATAGTTACAATAATACTCTTTCAAAT
CTTTTATGGCAGCAATAAAATAGTAATATTGTCTATTTTTTTGAGACTATTTTCACACAT
ATTTTAGAAACCCCTGTATCCTTCAGAATTACTGCGACTTAACGGAGAAATATATAGTA
TAATCCCACATTTTGTGAAAAAGACAAAGAATTAAGTAGTAGCTAATAATTGAACTAG
AACCAGAACCCTAAGAAATTTCTGACCCAAGCATATTATCTCTTTGGCTTAAGTGGTTC
CAGGTGAGGTTTCTTTAGAACGTAAAGCCTGAAATCACACCTTAAAAACACTTCCTTT
AACCTTTATAATTTCTTAATTTTACCATAAATGATTGCGTTTTATATTTACTGGGGCT
AACTAGNATTTTCTGNTATAGGTATTCTTTCCAACCTTTCTCTATTTTTTGTACTCAA
AGTGTAGTGGATGGACCGGAAGCATTGGGGTTCACCTGGGAGAATGGTTGGNAATGCAG
AACCCTTAGACCCCACCCAGCCCCTGTGAAA

Ref 10.2

Sequence of BAC9 using primer C3S12, which spans nucleotides 2909-29278 of the cDNA. Exon sequence is underlined and represents nucleotides 2931-2942.

CAGATAGTAGGTGAATGCTGTGGTGGTTCATAAAATGTCATCTTTAGTTTGTATTCTCT
CTGATGATTAGACTTTTCAGATCCAGATCTAATCATTTAGTAAGCCAGATCTTGCCAAAT
AAACTACTCCGTTAGAGAATAAGGACTTTTTAATAGTTACAATAATACTCTTCAAATCT
TTTATGGCAGCAATAAAATAGTAATATTGTCTATTTTTTTGAGACTATTTTACACATAT
TTTAGAAACCCCTGTATCCTTCAGAATTACTGCGACTTAACGGAGAAATATATAGTATA
ATCCACATTTTGTGAAAAGACAAAGAATTAAGTAGTAGCTAATAATTTGAACTAGA
ACCAGAACCCTAAGAAATTTCTGACCCAAGCATATTATCTCTTTGGCTTAACTGGTTCC
AGGNGAGGTATCTTTAGAACGTNAAAGCCTGAAATCACACCTTAAAAACACTTNCTTTA
ACCCTTTATAANTTNCTTAATTTTCACCATAAAATNGATTGCNGTTTTATATTTTACC
TNGGGNCTANACCTNAGGCAATTTTCTGGGTCATAAGGGAAATTTCTTTTCCCAAAC
CCTTTTCTTCTTATTTTGTGGGNCACCTCCCAAAGGTGNTCNGTTGGGGNTTNGGGN
CCCCGNGAAAGGCCATTTGGGGNTTCACCCCGGGGGANGATTTGGTTTTGGAAAATN
GTCNNNAAAACCTTCCNNACCCCNCCCCNCGGCCCCNTGNNNGGAAATCCAAAAGG
ATCTTGNCNATTTTTTTANCCAAANGANCNCCCCNAGGGNGGGATTTTNGTTATTTCC
CCAANAAGANGTAAGGTTNTTGGCCTTTNGGGGCNTTGGGTGTTTTNTTTNN

Ref 11.1

Bac 9 sequenced with HC3AS3, which spans nucleotides 3377-3394 of the cDNA. Exon sequence is underlined and represents nucleotides 3268-3290.

CTGANGTGTNGCAANGCCACTCCTGTGTCTTTTCTGCATGTCCTCAATAGCAACTTCAA
TCGGTGTTAAGATGATCTGAGTNANNGAGCATCTGTTANATCAGNGTACTGACTGAAAC
TATTTAATGAACTTTATGTATAATCAACTGAAATTAGANAAAAAAGATCAATNGTAA
ACTTCATGTAACAATAAAATTCCAAACTTGGATTCTAAATGAANNAAAAANATCAACCT
TTAAAGAAAAGCTGGGGTGAATAAGGGCTTAGAAAAGANGTANAAAATGANGACTCAA
AATGGTAAAGGGTCTAATATGNATGGATAAGGATGGACATATCTTCGGACTCTGAGTGG
TGTACATGGCTTGATGATTGCTCACTATGTGTGNCATTATGGCTACCTCTCTTTAGGCA
TGCCTGTTAANTAGGAAGCTGAACTANCAAAGNCTCTTNGATGTATNANTCCTGCCGCT
NAAGAAGGGGNCGCNTGANNCAAATGATTTGCNATGTNTCTGCTATNATNGNAAGNGNT
CCTNGANTNNTTCNGANAAANCTCTCNANGAGNCTAGTTTACATNCGGTGAGNGCTTCT
TGCACCTCCTGNGCATCTCCCGTANTTCACCCTCATTNNAACNTNANTTTATAANNANN
NAGCCACNTNNCCTATAGGCNATCNACGCNNTTCCNNTANTCANTNNNAGACAATTT
TTTNNCGCCCCCTCCTNNTCCTTCTNNTTCCNCCNCCNCCCTNTNTCTNTNCCCC
CNCCNNTTCTTANCTTNCT

Ref 12.1

Sequence of BAC9 using primer C3S15, which spans nucleotides 3751-3770 of the cDNA. Exon sequence is underlined and represents nucleotides 3780-4119, and also represent the 3 terminus of the transcriptional unit.

TGTGAAAAGATCTATTGGAAAACAACATGGAATGGAATTCTGGAAATTATTATTNATTG
AAGAATGCAGTGGCCAAGAAAATATCAAATGTAGATTGTTAACGCTTGAGAATCATGGC
TATGGTTTCTAATGTTCTGGTAACAAGCTGTTATCTTTTAAGACATTTTAATGACTCAA
AGGTACACTATACATTTACCATTATTTATACCATAGCTAAGGTTAAAAATTTATTTCACT
TTAAGTTCGTATTTTTTAATTTATATTACCATTTATAGATTCATTTTGGAACCATTTTA
AATGTAGTAATGCTTATTTTAAAGGTACTATTAAATATGTGAATGTTTACACTAATTTT
ACCGAGTGGGACTTCAAATTTTTATTATTGACAATGGCTGAGAACAATTNAAGGGTTT
GACTCNAGAACTANTTCCAAACCTAGCAGAATAAAAATCATAGATAGCCCCAAATTAAT
GAGTTTGGGNAACTGTNTCAAAGTTTTTTTCCATTTACATACCCAAAAACAGGAAATTT
TAGAATTTGCCNGAACCTTTACCTTAAGANAAAAACCCTTTTGTGNTNAAAAATNTANT
NTTAAAATTTCCCGGGGGGANTAATCTTAATNACCCCGGGTGGGGCCANNNCNCCCNTTA
TAACTTTGGAATTTAAAAATTCNTTTTTNTNCAACCCAAACTGNANTNGGGTNNTTT
TNAAGGAAAACCTTTCCACTNGGAAGTTNNCTTTTAGGGNCCNANCTNCNANAAANNG
GGGAANATTGGGAAGTCTTCCCCTTCNTTNGGGGGGNGNCCCAAAAAATTCTTAATAAA
ANCCCCGGGGCTCCCATNTTAGNATTTTTTTTTTTGGCCCCACACTGTGTTNATTAAA
NCCCCNCNTGCTAAAAATTTTTNNNGAAAAANACCTNAACCCTTCTNNA

HC2A	-----
KIAA	ASGNLDKNARFSAIYRQDSNKLSDMLKLLADFRKPEKMAKLPVILGNLDITIDNVSSD
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	-----
KIAA	FPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKHTQPYTIYTNHLYVYPKYLKYDSQ
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	-----VLHHHQNPETYDEIK
KIAA	KSFAKARNIAICIEFKDSDEEDSQPLKCIYGRPGGPVFTSAFAAVLHHHQNPETYDEIK
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	IELPTQLHEKHLLLLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPPLKDGRRVVTSEQHI
KIAA	IELPTQLHEKHLLLLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPPLKDGRRVVTSEQHI
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNNFFQYC
KIAA	PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNNFFQYC
rat	-----
HC4	-----
HC1	-----
HC3	-----GPGPARSTVSIISLISNSARV
HC5	-----
HC2A	QKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV
KIAA	QKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV
rat	-----
HC4	-----MEIQVLIRFLSVILMQLFWLPMIHEDDVPISCPMV
HC1	-----MSFLPIILNQLFKVLV-QNEEDEITTTVTRV
HC3	NRSRSLSNSNPDISGTPTS PDDEVRSIIGSKGLDRSNSWVNTGGPKAAPWGSNPSPSAES
HC5	-----

FIG. 4B (1 of 5)

Refs

HC2A	I IHVVAQCHEEGLESHLRSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSTN	
KIAA	I IHVVAQCHEEGLESHLRSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSTN	
rat	-----	
HC4	LFHIVSKCHEEGLDSYLSSFIKYSFRPGKPSAPQAPLIHETLATMMIALLKQSADFLAIN	
HC1	LPDIVAKCHEEQLDHSVQSYIKFVFKTR---ACKERPVEDLAKNVTGLLK-SNDSPTVK	
HC3	TQAMDRSCNRMSSTHTETSSFLQTLTGRLP----TKKLFHEELALQWVCSG--SVR---E	
HC5	-----	
	Cadherin	
	Cleavage	
HC2A	KLLRYSWFFFDVLIKSMAQHLENSKVKLLRNQRFPPASYHHAETVVNMLMPHITQKFGD	
KIAA	KLLKYSWFFFDVLIKSMAQHLENSKVKLLRNQRFPPASYHHAETVVNMLMPHITQKFRD	
rat	-----	
HC4	KLLKYSWFFFEIIAKSMATYLLLEENKIKLTHGQRFPPKAYHHAHSLFLAIT-IVESQYAE	
HC1	HVLKHSWFFFAIILKSMAQHLEIDTNKIQLERPPQRFPPESYQNELDNLMVLSHDHVIWKYKD	
HC3	SALQQAWFFFELMVKSMVHHLVFNDKLEAPRKSRFPFERFMDDIAALVSTIASDIVSRFQK	1.1/1.2/2.1/2.2
HC5	-----	
HC2A	NPEASKNANHSLAVFIKRCFTFMDRGFVFKQIN---NYIS--CFAPGDHKTLEFYKFEFL	
KIAA	NPEASKNANHSLAVFIKRCFTFMDRGFVFKQIN---NYIS--CFAPGDPKTLFEYKFEFL	
rat	-----	
HC4	IPKESRNVNYSLASFLKCCLTLMDRGFVFNLIN---DYIS--GFSPKDPKVLAEYKFEFL	
HC1	ALEETRRATHSVARFLKRCFTFMDRGCVFKMVN---NYIS--MFSSGDLKTLKQYKFDL	
HC3	DTEMVERLNTSLAFLNDLLSVMDRGFVFSLIKSCYKQVSSKLYSLPNPSVIIVSLRLDFL	3.1/3.2
HC5	-----	
HC2A	RVVCNHEHYIPLNLPM-----PFGKGRIQR-----YQDLQL---DYSLTDEF	
KIAA	RVVCNHEHYIPLNLPM-----PFGKGRIQR-----YQDLQL---DYSLTDEF	
rat	-----	
HC4	QTICNHEHYIPLNLPM-----AFAPKPKLQR-----VQDSNL---EYSLSDEY	
HC1	QEVQHEHFIPCLPIRSANIPDPLTPSES-----TQELHASDMPEYSVTNEF	
HC3	RIICSHHEYVTLNLPCLLTPPASPSVSSATISQSSGFSTNVQDQKIANMFELS--VPF	4.1/4.2
HC5	-----MNADTAPTSPCPSIS---SQNSSSCSSFQDQKIASMFDRTSRVPA	
	Cadherin	
	EC motif	
HC2A	CRNHFLVGLLLREVG TALQEFRE---VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT	
KIAA	CRNHFLVGLLLREVG TALQEFRE---VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT	
rat	-----	
HC4	CKHHFLVGLLLRETSIALQDNYE---IRYTAISVIKNLLIKHAFDTRYQHKNQQAQIAQ	
HC1	CRKHFLIGILLREVG FALQEDQD---VRHLALAVLKNLMAKHSFDDRYREPRKQAQIAS	
HC3	RQQHYLAGLVLT ELAVILDPAEGLFGLHKKVINMVHNLSSHSDSDPRYSDPQIKARVAM	
HC5	SSTS-SPGLLFTELAALDAEGEGISEVQRKAVSAIHSLLSSHDLDPKVCVPEVKVIAA	
HC2A	LYLPLFGLLIENVQRINVRDVSPFPVNAG-MTVKDESLALPAVNPLVTPQKGSTLDNSLH	
KIAA	LYLPLFGLLIENVQRINVRDVSPFPVNAG-MTVKDESLALPAVNPLVTPQKGSTLDNSLH	
rat	-----	
HC4	LYLPPFVGLLLENIQRLAGRDTLYSCAAMPNSASRDEFPCG-----FTSP--AN--RGSLS	
HC1	LYMPLYGMLLDNMPRIYKDLYPFTVNTSNQGSRDDLS TNGGFQSQTAIKHANSVDTSFS	
HC3	LYLPLIGIIMETVPQLYDFTETHNQGRPICIA TDDYESE-----SG---SMIS	
HC5	LYLPLVGII LDALPQLCDFTVADTRRYR---TSGSDEEQE-----GA---GAIT	

FIG. 4B (2 of 5)

		Refs
HC2A	KDLLGAISGIAASPYTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQSS	
KIAA	KDLLGAISGIAASPYTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQSS	
rat	-----	
HC4	TDKDTAYGSFQNG-----HGIKREDSRGSLIP-EGATGFDPQGNTGEN-----TRQS	
HC1	KDVLNSIAAFSS-----IAISTVNHADSRASLASLDSNPSTNEKSSEKTDNCEKIPRPL	
HC3	QTVAMAIAGTSVPQ-----LTRPGSFLLTSTSGRQHT-----	5.1/5.2
HC5	QNVALAIAGNNFN-----LKTSG-IVLSSLPYKQYN-----	
HC2A	TLGNSVVRCDKLDQSEIKSLLMCFLYILKSMSDDALFTYWN-KASTSELMDFFTISEVCL	
KIAA	TLGNSVVRCDKLDQSEIKSLLMCFLYILKSMSDDALFTYWN-KASTSELMDFFTISEVCL	
rat	-----	
HC4	STRSSVSQYNRLDQYEIRSLLMCYLYIVKMISEDTLITYWN-KVSPQELINILILEVCL	
HC1	ALIGSTLRFDRLDQAETRSLLMCFLHIMKTISYETLIAYWQ-RAPSPEVSDFFSIIIVCL	
HC3	-----TFSAESSRSLICLLWVLKN-ADETVLQKWFTDLSVLQNLRLDLLYLVCV	
HC5	-----MLNADTTRNLMICFLWIMKN-ADQSLIRKWIADLPSTQLNRLDLLFICV	
HC2A	HQFYMGKRYIARNQEGLG--PIVHDRKS-----QTLPVSRNRTGMM	
KIAA	HQFYMGKRYIAR-----TGMM	
rat	-----	
HC4	FHFRYMGRNIARVHDAWLSKHFGIDRKS-----QTMPALNRNRSGVM	
HC1	QNFYRLGKRNIIRKIAAAF--KFVQSTQNNGTLKGSNPSCQTSGLLAQWMHSTSRHEGK	
HC3	SCFEYKGGKVFERNMSTLTFK--KSKDMRAK-----LEEAILGSIGARQEMV	
HC5	LCFEYKGGKQSSDKVSTQVLQ--KSRDVKAR-----LEEALLRGEARGEMM	
HC2A	HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC	
KIAA	HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC	
rat	-----	
HC4	QARLQHL-----SSLESS-----FTLNHSSTTEADIFHQALLEGNTATEVS	
HC1	QHRSQLPIIRGK--NALSNPKL--LQMLDNTMTSNEIDIVHHVDTEANITEGC	
HC3	RRSRGQLERSPSGSAFGSQENLRWKDMTHWRQNTKLDKSRAEIEHEALIDGNLATEAN	6.1/6.2
HC5	RRRAPGNDRFP--GLNENLRWKKEQTHWRQANEKLDKTKAELDQEALISGNLATEAH	
HC2A	LTALDTLSLFTLAFKNQLLADHGHNPMLKKVFDVYLCFLQKHQSETALKNVFTALRSLIY	
KIAA	LTALDTLSLFTLAFKNQLLADHGHNPMLKKVFDVYLCFLQKHQSETALKNVFTALRSLIY	
rat	-----KLSRGHSPMLKKVFDVYLCFLQKHQSEMAKKNVFTALRSLIY	
HC4	LTVLDTISFFTQCFKTHFLNNDGHNPMLKKVFDIHLAFLKNGQSEVSLKHVFASLRAFIS	
HC1	LTILDVLSLFTQTHQRQLQQCDQNSLMKRGFDTYMLFFQVQNSATALKHVFASLRLFVC	
HC3	LIILDTLEIVVQTVS--VTES--KESILGGVLKVLHSMACNSAVYLVQHCFAQRALVS	
HC5	LIILDMQENIIQASS--ALDC--KDSLLGGVLRVLVNSLNCQSTTYLTHCFATLRLALIA	
HC2A	KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH	
KIAA	KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH	
rat	KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH	
HC4	KFPFAFFKGRVNMCAAFCEYVLKCCSTKISSTRNEASALLYLLMRNNFEYTKRKTFLRTH	
HC1	KFPFAFFQGPADLCGSFCYEVVLKCCNHRSRSTQTEASALLYLFMRKNFEFNKQKSIVRSH	
HC3	KFPPELLFEEETEQCADLCLRLLRHCCSSSIGTIRSHPSASLYLLMRQNFEIGN--NFARVK	7.1/7.2
HC5	KFGDLLFEEVEQCFDLCHQVLHHCSSSMDVTRSQCATLYLLMRFSFGATS--NFARVK	
HC2A	LQVIIISVSQLIADVVGIGETRFQQSLSIINNANCANDRLIKHTSFSSDVKDLTRIRTVLM	
KIAA	LQVIIISVSQLIADVVGIGGTRFQQSLSIINNANCANDRLIKHTSFSSDVKDLTRIRTVLM	
rat	LQVIIISVSQLIADVVGIGGTRFQQSLSIINNANCANDRLIKHTSFSSDVKDLTRIRTVLM	
HC4	LQIIIAVSQLIADVALSGGSRFQESLFIINNANFANDRPMLARAFPAEVKDLTRIRTVLM	
HC1	LQLIKAVSQLIAD-AGIGGSRFQHS LAITNNFANGDKQMKNSNFPFAEVKDLTRIRTVLM	
HC3	MQVPMSSLVSGTSQNFNEEFLRRSLKTIITYAEDLELRETTFPDQVQDLVFNLMILS	
HC5	MQVTMSLASLVGRAPDFNEEHLRRSLRTILAYSEEDTAMQMTFPPTQVEELLCNLNSILY	

FIG. 4B (3 of 5)

	Transmembrane		
HC2A	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKRWLDSMARIHVKNGD	LSEAMCYVHV	
KIAA	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKRWLDSMARIHVKNGD	LSEAMCYVHV	
rat	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKRWLDSMARIHVKNGD	LSEAMCYVHV	
HC4	ATAQMKEHEKDPEMLIDLQYSLAKSYASTPELRKRWLDSMAKIHVKNGD	FSEAMCYVHV	
HC1	ATAQMKEHEKDPEMLVDLQYSLANSYASTPELRRTWLDSMAKIHARNGD	LSEAMCYIHI	
HC3	DTVKMKEHQEDPEMLIDLMYRIAKGYQTSPDLRLTLWLQNMAGKHSERSN	HAEAAQCLVHS	
HC5	DTVKMREFQEDPEMLMDLMYRIAKSYQASPDRLTLWLQNMAEKHTKKKC	YTEAMCLVHA	
HC2A	TALVAEYL	TRKGV	-----FRQGCTAFRVITPN
KIAA	TALVAEYL	TRKEA	-----VQWEPPLPHSHSACLRRSRGGVFROGCTAFRVITPN
rat	TALVAEYL	TRKEAD	-----LALQREPPVPFPYSHTSCQRKSRGGMFRQGCTAFRVITPN
HC4	AALVAEFL	HRKKL	-----FPNGCSAFKKITPN
HC1	AALIAEYL	KRKGWKVEKIC	TASLLSEDTHPCDNSNLLTTPSGGSMFSGMGPAPFLSITPN
HC3	AALVAEYL	SMLLED	-----RKYLPVGCVTFDNISSN
HC5	AALVAEYL	SMLLED	-----HSYLPVGSVSFQNISSN
HC2A	IDEEASMMEDVGMQD	-----VHFNEDVLMELLEQCADGLWKAERYELIADIYKLI	IPI
KIAA	IDEEASMMEDVGMQD	-----VHFNEDVLMELLEQCADGLWKAERYELIADIYKLI	IPI
rat	IDEEASMMEDVGMQD	-----VHFNEDVLMELLEQCADGLWKAERLRAGLLTSINSSSP	
HC4	IDEEGAMKEDAGMMD	-----VHYSEEVLLLELLEQCVNGLWKAERYEII	SEISKLIGPI
HC1	IKEEGAAKEDSGMHD	-----TPYNEINILVEQLYMCGEFLWKSERVELI	ADVNKPIIAV
HC3	VLEESAVSDDVVPDEEGICSGKYFTESGLVGLLEQAAASF	SMAGMYEAVNEVYKVL	IPI
HC5	VLEESVVSIEDTLSPDEDGVCAGQYFTESGLVGLLEQAELF	STGGLYETVNEVYKVL	IPI
HC2A	YEKRRD	-----	
KIAA	YEKRRD	FERLAHLYDTLHRAYSKVTEVMHSGRRLGTYFRVAFFGQAAQYQFTDSETDVE	
rat	SMKSGGTLETHLYDTLHRPYSKVTEVITR	-----A-----AGSWDLLPGGLFGQ	
HC4	YENRREFENLTQVYRTIHGAYTKILEVMHTKKRLLG	-----TFFRVAFYGO	
HC1	FEKQDFKKLSDLYYDIHRSYLVKVAEVDNSEKRLFG	-----RYFRVAFYGO	
HC3	HEANRDAKKLSTIHGKLQEAFSKIVHGSTGWERMFG	-----TYFRVGFYGO	
HC5	LEAHREFRKLTLTHSKLQRAFDIVNKH--KRMFG	-----TYFRVGFYGO	
HC2A	-FFEDDGKEYIYKEPKLTPLSEISQRLCLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYA		
KIAA	GFFEDDGKEYIYKEPKLTPLSEISQRLCLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYA		
rat	GFFEDDGKEYIYKEPKLTPLSEISQRLCLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYA		
HC4	SFFEEEDGKEYIYKEPKLTGLSEISLRVLKLYGEKFGTENVKIIQSDKVNKELDPKYA		
HC1	GFFEEEGKEYIYKEPKLTGLSEISQRLCLKLYADKFGADNVKIIQDSKNVNPKDLDPKYA		
HC3	TKFGDLDEQEFVYKEPAITKLAEISHRIEFGFYGERFGEDVVEVIKDSNPVDCKLDPNKA		
HC5	SKFGDLDEQEFVYKEPAITKLPEISHRLEAFYGCFCGAEFVEVIKDSNPVDKTKLDPNKA		
HC2A	YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVVEEQCKRRTILTA		
KIAA	YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVVEEQCKRRTILTA		
rat	YIQVTHVTPFFDEKELQERKTEFERCHNIRRFMFEMPFTQTGKRQGGVVEEQCKRRTILTA		
HC4	HIQVTVYVVPYFDDKELTERKTEFERNHNISRFVFEAPYTLGKKQGCIEEQCKRRTILT		
HC1	YIQVTVYVTPFFEEKEIEDRKTD FEMHHNINRFVFETPFTLSGKKHGGVVAEQCKRRTILT		
HC3	YIQITYVEPYFDTYEMKDRITYFDKNYNLRRFMYCTPFTLDGRAHGEQFQRKTILT		
HC5	YIQITTFVEPYFDEYEMKDRVITYFEKNFNLRRFMYTTPFTLEGRPRGELHEQYRRNTVLTT		

8.1/8.2

9.1

10.1/10.2

FIG. 4B (4 of 5)

		Coiled-Coil 1	Refs
HC2A	IHCFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQGSV		
KIAA	IHCFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQGSV		
rat	IHCFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELHQLCSSAEVDMIKLQLKLQGSV		
HC4	SNSFPYVKKRIPINCEQQINLKPIDGATDEIKDKTAELOKLCSSTDVDMIQQLKLQGWV		
HC1	SHLFPYVKKRIQVISQSSTELNPIEVAIDEMSRKVSELNQLCTMEEVDMISLQLKLQGSV		
HC3	SHAFPIKTRVNVTHKEIILTPIEVAIDMQKKTQELAFATHQDPADPKMLQMVLQGSV		11.1
HC5	MHAFPIKTRISVIQKEEFVLTPIEVAIDEMKKKTLQLAVAINQEPDAKMLQMVLQGSV		
		Coiled-Coil 2	
HC2A	SVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLE		
KIAA	SVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLE		
rat	SVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLE		
HC4	SVQVNAGPLAYARAFLLDSQASKYPPKKVSELKDMFRKFIQACSIASELNERLIKEDQVE		
HC1	SVKVNAGPMAYARAFLEETNAKKYPDNQVKLLKEIFRQFADACGQALDVNERLIKEDQLE		
HC3	GTTVNQGPLEVAQVFLSEIPSDPKLFRHHNKLRLCFKDFTKRCEDALRKNKSLIGPVQKE		
HC5	GATVNQGPLEVAQVFLAEIPADPKLYRHHNKLRLCFKEFIMRCGEAVEKNKRLITADQRE		
		Coiled-Coil 2	
HC2A	YQEEMKANYREMAKELSEIMHEQICPLEEKTS-VLPNSLHIFNAISGTPSTMTVHGMTSS		
KIAA	YQEEMKANYREMAKELSEIMHEQLG-----		
rat	YQEEMKANYREIRKELSDIIVPRICPGEDKRATKFPAPHLQRHQRTDNKHSGSRVDQFILS		
HC4	YHEGLKSNFRDMVKELSDIIEHQILQEDTMHSPWMSNTLHVFCIAISGTSSDRGYGSPRYA		
HC1	YQEELRSHYKMDLSELSTVMNEQITGRDDLK---RGVDQTCTRVISKATPALPTVSISS		
HC3	YQRELG---KLSS-----P-----		
HC5	YQQELKKNYNKLKENLRPMIERKIPELYKPIFRVESQKRDSFHRSSFRKCETQLSQGS--		
		PBM	
HC2A	SSVV-----		
KIAA	-----		
rat	CVTLPHPEPHVGTCFVMCKLRTTFRANHWFCQAQEEAMGNGREKEPWTVIFNSRFYRSWGK		
HC4	EV-----		
HC1	SAEV-----		
HC3	-----		
HC5	-----		
HC2A	-----		
KIAA	-----		
rat	VHIFF		
HC4	-----		
HC1	-----		
HC3	-----		
HC5	-----		

FIG. 4B (5 of 5)

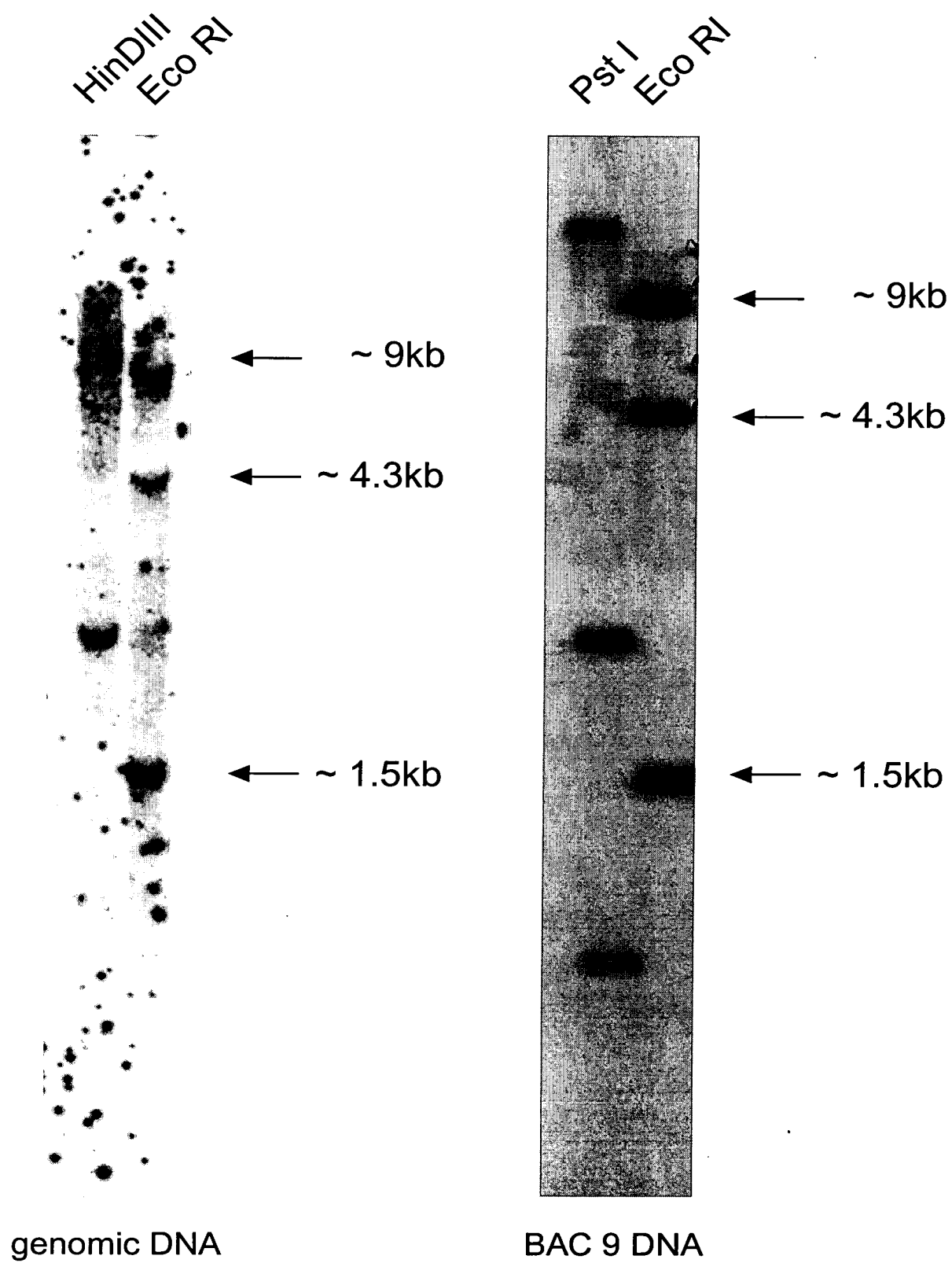


FIG. 5

-21

GTCGCCGTCGCCGAGCAGCC -1

1/1	31/11
ATG GCC GAG CGC CGC GCC TTC GCC CAG AAG	ATC AGC AGA ACG GTG GCA GCC GAA GTT AGG
Met ala glu arg arg ala phe ala gln lys	ile ser arg thr val ala ala glu val arg
61/21	91/31
AAG CAG ATC TCC GGA CAA TAT AGT GGT TCT	CCC CAA CTG CTC AAA AAC CTT AAT ATT GTT
lys gln ile ser gly gln tyr ser gly ser	pro gln leu leu lys asn leu asn ile val
121/41	151/51
GGC AAT ATA TCC CAT CAC ACC ACA GTG CCC	CTT ACC GAA GCA GTA GAT CCA GTG GAT TTG
gly asn ile ser his his thr thr val pro	leu thr glu ala val asp pro val asp leu
181/61	211/71
GAA GAT TAC CTC ATT ACT CAT CCT TTG GCT	GTG GAT TCT GGG CCT TTA CGG GAT TTG ATT
glu asp tyr leu ile thr his pro leu ala	val asp ser gly pro leu arg asp leu ile
241/81	271/91
GAA TTT CCT CCA GAT GAT ATT GAA GTT GTT	TAT AGT CCT CGG GAC TGC AGA ACT CTT GTT
glu phe pro pro asp asp ile glu val val	tyr ser pro arg asp cys arg thr leu val
301/101	331/111
TCA GCT GTA CCT GAA GAA AGT GAA ATG GAT	CCA CAT GTT AGA GAC TGT ATA AGA AGT TAT
ser ala val pro glu glu ser glu met asp	pro his val arg asp cys ile arg ser tyr
361/121	391/131
ACA GAA GAC TGG GCA ATT GTC ATC AGA AAA	TAT CAT AAA TTG GGA ACA GGA TTT AAT CCC
thr glu asp trp ala ile val ile arg lys	tyr his lys leu gly thr gly phe asn pro
421/141	451/151
AAT ACA TTA GAT AAA CAG AAA GAA AGG CAA	AAA GGT TTG CCA AAA CAA GTT TTT GAA TCT
asn thr leu asp lys gln lys glu arg gln	lys gly leu pro lys gln val phe glu ser
481/161	511/171
GAT GAA GCT CCA GAT GGC AAC AGC TAC CAG	GAT GAT CAA GAT GAC CTT AAA AGA CGT TCA
asp glu ala pro asp gly asn ser tyr gln	asp asp gln asp asp leu lys arg arg ser
541/181	571/191
ATG TCA ATA GAT GAT ACC CCA AGG GGT AGC	TGG GCC TGT AGT ATC TTT GAC TTG AAA AAT
met ser ile asp asp thr pro arg gly ser	trp ala cys ser ile phe asp leu lys asn
601/201	631/211
TCA CTT CCT GAT GCT TTG CTT CCC AAT TTA	CTT GAT CGA ACT CCA AAT GAA GAA ATA GAC
ser leu pro asp ala leu leu pro asn leu	leu asp arg thr pro asn glu glu ile asp
661/221	691/231
CGT CAG AAT GAT GAC CAA AGG AAA TCA AAC	CGT CAC AAA GAA CTT TTT GCT TTG CAT CCA
arg gln asn asp asp gln arg lys ser asn	arg his lys glu leu phe ala leu his pro
721/241	751/251
TCA CCA GAT GAG GAA GAA CCA ATA GAA CGG	CTT AGT GTT CCT GAT ATA CCC AAA GAA CAT
ser pro asp glu glu glu pro ile glu arg	leu ser val pro asp ile pro lys glu his
781/261	811/271
TTT GGT CAA AGA CTT CTT GTA AAA TGC TTA	TCA CTC AAG TTT GAA ATT GAA ATT GAA CCC
phe gly gln arg leu leu val lys cys leu	ser leu lys phe glu ile glu ile glu pro
841/281	871/291
ATT TTT GCA AGT TTG GCT TTA TAT GAT GTC	AAG GAA AAG AAA AAG ATT TCA GAA AAC TTT
ile phe ala ser leu ala leu tyr asp val	lys glu lys lys lys ile ser glu asn phe
901/301	931/311
TAT TTT GAC CTT AAT TCT GAG CAG ATG AAA	GGG TTG TTA CGT CCA CAT GTA CCA CCT GCT
tyr phe asp leu asn ser glu gln met lys	gly leu leu arg pro his val pro pro ala
961/321	991/331
GCC ATT ACT ACC CTG GCA AGA TCA GCA ATT	TTT TCT ATC ACT TAT CCT TCC CAA GAT GTT
ala ile thr thr leu ala arg ser ala ile	phe ser ile thr tyr pro ser gln asp val

FIG. 6A (1 of 6)

1021/341	TTT CTT GTA ATA AAG CTA GAA AAA GTC CTA	1051/351	CAG CAA GGA GAC ATT GGA GAG TGT GCA GAA
phe leu val ile lys leu glu lys val leu	1081/361	1111/371	gln gln gly asp ile gly glu cys ala glu
CCA TAT ATG ATT TTC AAA GAA GCA GAT GCC	1141/381	1171/391	ACC AAG AAT AAA GAA AAA CTG GAG AAA CTG
pro tyr met ile phe lys glu ala asp ala	1201/401	1231/411	thr lys asn lys glu lys leu glu lys leu
AAG AGT CAA GCA GAT CAG TTT TGC CAA AGA	1261/421	1291/431	CTT GGG AAA TAT CGC ATG CCT TTT GCT TGG
lys ser gln ala asp gln phe cys gln arg	1321/441	1351/451	leu gly lys tyr arg met pro phe ala trp
ACT GCA ATC CAT TTA ATG AAT ATT GTT AGC	1381/461	1411/471	AGT GCT GGG AGT TTG GAA AGA GAT TCT ACA
thr ala ile his leu met asn ile val ser	1441/481	1471/491	ser ala gly ser leu glu arg asp ser thr
GAA GTA GAA ATC AGT ACT GGA GAA CGA AAA	1501/501	1531/511	GGG TCT TGG TCA GAG AGG AGG AAT TCT AGT
glu val glu ile ser thr gly glu arg lys	1561/521	1591/531	gly ser trp ser glu arg arg asn ser ser
ATT GTT GGC AGA CGA TCA CTT GAA AGG ACA	1621/541	1651/551	ACA AGT GGA GAT GAT GCT TGT AAC TTG ACG
ile val gly arg arg ser leu glu arg thr	1681/561	1711/571	thr ser gly asp asp ala cys asn leu thr
AGC TTT CGA CCA GCT ACT CTC ACA GTG ACA	1741/581	1771/591	AAT TTT TTT AAG CAG GAA GGA GAC CGC TTA
ser phe arg pro ala thr leu thr val thr	1801/601	1831/611	asn phe phe lys gln glu gly asp arg leu
AGT GAT GAA GAT CTC TAC AAA TTC CTT GCT	1861/621	1891/631	GAT ATG AGA AGG CCA TCT TCT GTC TTA CGG
ser asp glu asp leu tyr lys phe leu ala	1921/641	1951/651	asp met arg arg pro ser ser val leu arg
CGA CTA AGA CCT ATT ACA GCT CAG CTC AAG	1981/661	2011/671	ATA GAC ATT TCT CCC GCA CCT GAA AAT CCC
arg leu arg pro ile thr ala gln leu lys	2041/681	2071/691	ile asp ile ser pro ala pro glu asn pro
CAT TAT TGC CTA ACT CCG GAG CTG CTT CAA	2101/701	2131/711	GTG AAG CTT TAC CCT GAC AGT AGA GTT AGA
his tyr cys leu thr pro glu leu leu gln			val lys leu tyr pro asp ser arg val arg
CCT ACC AGA GAA ATC TTA GAG TTT CCC GCA			AGG GAT GTT TAT GTT CCA AAC ACT ACT TAC
pro thr arg glu ile leu glu phe pro ala			arg asp val tyr val pro asn thr thr tyr
AGA AAT CTT CTC TAC ATA TAC CCT CAG AGT			1711/571
arg asn leu leu tyr ile tyr pro gln ser			CTT AAT TTT GCC AAT CGT CAA GGT TCT GCT
AGA AAT ATA ACA GTG AAA GTC CAG TTT ATG			leu asn phe ala asn arg gln gly ser ala
arg asn ile thr val lys val gln phe met			1771/591
GTA ATC TTT GGT AAA TCT AGC TGT TCA GAA			TAT GGA GAG GAT CCA AGC AAT GCC ATG CCG
val ile phe gly lys ser ser cys ser glu			tyr gly glu asp pro ser asn ala met pro
TAT CAT AAC AGG TCT CCT GAT TTT CAT GAA			1831/611
tyr his asn arg ser pro asp phe his glu			TTT TCA AAG GAA GCC TAT ACA GCC GTA GTA
ACT GAC CAT CAT CAC TTG CTT TTT ACT TTT			phe ser lys glu ala tyr thr ala val val
thr asp his his his leu leu phe thr phe			1891/631
ACT CCT CTT GAA ACA CCA GTT GGA TAT ACA			GAA ATC AAG GTT AAG CTT CCT GCT ACT TTA
thr pro leu glu thr pro val gly tyr thr			glu ile lys val lys leu pro ala thr leu
AAG ACT GGC CAG TTT TGC TTG CCA GTC TCA			1951/651
lys thr gly gln phe cys leu pro val ser			TAT CAT GTT AGT TGT CAA CAA AAA CAA AAT
CTG TCT CCT GAG GTT CCT CTA CCT GGC ATG			tyr his val ser cys gln gln lys gln asn
leu ser pro glu val pro leu pro gly met			2011/671
			TGG ATA CCA ATG CTT CAG AAT GGA CGG TTG
			trp ile pro met leu gln asn gly arg leu
			2071/691
			TTG GAA AAA CCA CCA CAG GCT TAT TCT GTA
			leu glu lys pro pro gln ala tyr ser val
			2131/711
			AAA TGG GTA GAT AAT CAC AAA GGT GTT TTT
			lys trp val asp asn his lys gly val phe

FIG. 6A (2 of 6)

3301/1101	GTG TCT TCA AAG CTT TAC TCA TTA CCG AAT	3331/1111	CCC AGT GTT CTG GTG TCC TTG AGG CTG GAT
	val ser ser lys leu tyr ser leu pro asn		pro ser val leu val ser leu arg leu asp
3361/1121	TTT CTA CGA ATC ATC TGC AGT CAT GAG CAC	3391/1131	TAT GTT ACA TTA AAC TTA CCC TGC AGC TTA
	phe leu arg ile ile cys ser his glu his		tyr val thr leu asn leu pro cys ser leu
3421/1141	CTT ACT CCA CCT GCA TCT CCA TCA CCT TCT	3451/1151	GTT TCT TCT GCA ACA TCT CAG AGT TCT GGA
	leu thr pro pro ala ser pro ser pro ser		val ser ser ala thr ser gln ser ser gly
3481/1161	TTT TCT ACG AAT GTA CAA GAC CAA AAG ATT	3511/1171	GCA AAT ATG TTT GAA TTA TCC GTG CCT TTC
	phe ser thr asn val gln asp gln lys ile		ala asn met phe glu leu ser val pro phe
3541/1181	CGC CAA CAG CAT TAT TTG GCA GGA CTT GTG	3571/1191	TTA ACA GAG CTG GCT GTC ATT TTA GAC CCT
	arg gln gln his tyr leu ala gly leu val		leu thr glu leu ala val ile leu asp pro
3601/1201	GAT GCT GAA GGA CTG TTT GGA TTG CAT AAG	3631/1211	AAA GTC ATC AAT ATG GTA CAC AAT TTA CTC
	asp ala glu gly leu phe gly leu his lys		lys val ile asn met val his asn leu leu
3661/1221	TCC AGT CAC GAC TCA GAC CCG CGG TAC TCT	3691/1231	GAC CCT CAG ATA AAG GCT CGA GTG GCC ATG
	ser ser his asp ser asp pro arg tyr ser		asp pro gln ile lys ala arg val ala met
3721/1241	TTG TAT CTA CCT CTG ATT GGT ATT ATC ATG	3751/1251	GAA ACT GTA CCT CAG CTG TAT GAT TTT ACA
	leu tyr leu pro leu ile gly ile ile met		glu thr val pro gln leu tyr asp phe thr
3781/1261	GAA ACT CAC AAT CAA CGA GGA AGA CCA ATT	3811/1271	TGT ATA GCC ACT GAT GAT TAT GAA AGT GAG
	glu thr his asn gln arg gly arg pro ile		cys ile ala thr asp asp tyr glu ser glu
3841/1281	AGC GGA AGT ATG ATA AGC CAG ACC GTT GCC	3871/1291	ATG GCA ATC GCA GGG ACA TCG GTC CCT CAA
	ser gly ser met ile ser gln thr val ala		met ala ile ala gly thr ser val pro gln
3901/1301	CTA ACA AGG CCT GGC AGT TTC CTC CTC ACG	3931/1311	TCA ACG AGT GGC AGG CAA CAC ACT ACC TTT
	leu thr arg pro gly ser phe leu leu thr		ser thr ser gly arg gln his thr thr phe
3961/1321	TCA GCA GAA TCA AGT CGA AGC CTT TTG ATC	3991/1331	TGT CTA CTT TGG GTT CTC AAA AAT GCA GAT
	ser ala glu ser ser arg ser leu leu ile		cys leu leu trp val leu lys asn ala asp
4021/1341	GAA ACA GTT CTA CAG AAG TGG TTT ACA GAT	4051/1351	CTC TCA GTC TTG CAG CTA AAC CGG CTA TTA
	glu thr val leu gln lys trp phe thr asp		leu ser val leu gln leu asn arg leu leu
4081/1361	GAT CTG CTT TAT CTC TGT GTG TCT TGC TTT	4111/1371	GAG TAT AAA GGG AAA AAA GTG TTT GAA CGA
	asp leu leu tyr leu cys val ser cys phe		glu tyr lys gly lys lys val phe glu arg
4141/1381	ATG AAT AGC TTG ACC TTT AAG AAA TCA AAA	4171/1391	GAC ATG AGA GCA AAG CTT GAA GAA GCT ATT
	met asn ser leu thr phe lys lys ser lys		asp met arg ala lys leu glu glu ala ile
4201/1401	CTT GGG AGC ATA GGT GCC AGG CAA GAA ATG	4231/1411	GTA CGG CGA AGC CGA GGA CAG CTC GAG AGA
	leu gly ser ile gly ala arg gln glu met		val arg arg ser arg gly gln leu glu arg
4261/1421	AGC CCA TCT GGA AGT GCC TTT GGA AGT CAA	4291/1431	GAA AAT TTG AGG TGG AGG AAA GAT ATG ACT
	ser pro ser gly ser ala phe gly ser gln		glu asn leu arg trp arg lys asp met thr
4321/1441	CAC TGG CGT CAA AAC ACA GAG AAG CTT GAC	4351/1451	AAA TCA AGA GCA GAG ATT GAA CAC GAA GCA
	his trp arg gln asn thr glu lys leu asp		lys ser arg ala glu ile glu his glu ala
4381/1461	CTG ATT GAT GGA AAC CTG GCT ACA GAA GCA	4411/1471	AAC CTA ATC ATT TTA GAT ACA TTA GAG ATT
	leu ile asp gly asn leu ala thr glu ala		asn leu ile ile leu asp thr leu glu ile

FIG. 6A (4 of 6)

4441/1481	GTT GTT CAG ACC GTT TCT GTA ACG GAA TCC	4471/1491	AAA GAG AGC ATT CTT GGT GGA GTG CTA AAA
val val gln thr val ser val thr glu ser	lys glu ser ile leu gly gly val leu lys		
4501/1501	GTG CTA CTA CAC AGC ATG GCC TGT AAC CAA	4531/1511	AGT GCA GTT TAT CTA CAA CAC TGT TTT GCT
val leu leu his ser met ala cys asn gln	ser ala val tyr leu gln his cys phe ala		
4561/1521	ACA CAG AGA GCC TTG GTT TCA AAG TTT CCT	4591/1531	GAA CTC TTA TTT GAA GAA GAG ACA GAG CAG
thr gln arg ala leu val ser lys phe pro	glu leu leu phe glu glu glu thr glu gln		
4621/1541	TGT GCT GAT TTA TGC CTC AGG CTT CTC CGA	4651/1551	CAC TGT AGC AGT AGC ATC GGT ACA ATA CGG
cys ala asp leu cys leu arg leu leu arg	his cys ser ser ser ile gly thr ile arg		
4681/1561	TCA CAC CCC AGT GCC TCC CTT TAC CTA CTA	4711/1571	ATG AGG CAA AAC TTT GAG ATT GGG AAT AAC
ser his pro ser ala ser leu tyr leu leu	met arg gln asn phe glu ile gly asn asn		
4741/1581	TTT GCC AGG GTT AAA ATG CAG GTA CCA ATG	4771/1591	TCA CTA TCC TCC TTG GTG GGC ACA TCT CAG
phe ala arg val lys met gln val pro met	ser leu ser ser leu val gly thr ser gln		
4801/1601	AAT TTT AAT GAA GAA TTC TTA AGA CGT TCT	4831/1611	CTA AAG ACT ATA TTG ACA TAT GCT GAA GAA
asn phe asn glu glu phe leu arg arg ser	leu lys thr ile leu thr tyr ala glu glu		
4861/1621	GAT CTG GAA TTG AGG GAA ACA ACA TTT CCT	4891/1631	GAT CAG GTC CAG GAT CTG GTT TTC AAT CTC
asp leu glu leu arg glu thr thr phe pro	asp gln val gln asp leu val phe asn leu		
4921/1641	CAT ATG ATT CTT TCT GAT ACT GTG AAA ATG	4951/1651	AAG GAA CAC CAG GAG GAT CCT GAA ATG TTG
his met ile leu ser asp thr val lys met	lys glu his gln glu asp pro glu met leu		
4981/1661	ATT GAT CTA ATG TAC AGA ATT GCC AAG GGT	5011/1671	TAC CAG ACC TCT CCA GAG CGA TTG ACC TGG
ile asp leu met tyr arg ile ala lys gly	tyr gln thr ser pro glu arg leu thr trp		
5041/1681	TTG CAG AAC ATG GCA GGC AAG CAC TCA GAA	5071/1691	CGA AGC AAT CAT GCT GAA GCT GCA CAG TGT
leu gln asn met ala gly lys his ser glu	arg ser asn his ala glu ala ala gln cys		
5101/1701	CTA GTC CAC TCA GCA GCA CTT GTT GCT GAA	5131/1711	TAT TTG AGC ATG CTG GAG GAC CGG AAA TAT
leu val his ser ala ala leu val ala glu	tyr leu ser met leu glu asp arg lys tyr		
5161/1721	CTT CCT GTG GGA TGT GTA ACA TTT CAG AAT	5191/1731	ATT TCA TCT AAT GTT TTA GAA GAA TCT GCG
leu pro val gly cys val thr phe gln asn	ile ser ser asn val leu glu glu ser ala		
5221/1741	GTC TCA GAT GAT GTG GTA TCT CCA GAT GAA	5251/1751	GAA GGT ATC TGC TCT GGA AAA TAC TTT ACT
val ser asp asp val val ser pro asp glu	glu gly ile cys ser gly lys tyr phe thr		
5281/1761	GAG TCA GGA CTT GTG GGA TTA CTG GAA CAA	5311/1771	GCA GCT GCT TCC TTC TCT ATG GCT GGC ATG
glu ser gly leu val gly leu leu glu gln	ala ala ala ser phe ser met ala gly met		
5341/1781	TAT GAA GCA GTT AAT GAA GTT TAC AAA GTA	5371/1791	CTT ATT CCT ATT CAT GAA GCT AAT CGG GAT
tyr glu ala val asn glu val tyr lys val	leu ile pro ile his glu ala asn arg asp		
5401/1801	GCA AAG AAA CTA TCC ACA ATT CAT GGT AAA	5431/1811	CTT CAA GAA GCA TTC AGC AAA ATT GTT CAT
ala lys lys leu ser thr ile his gly lys	leu gln glu ala phe ser lys ile val his		
5461/1821	CAG AGT ACT GGC TGG GAG CGG ATG TTT GGC	5491/1831	ACC TAT TTT CGT GTT GGT TTT TAT GGA ACC
gln ser thr gly trp glu arg met phe gly	thr tyr phe arg val gly phe tyr gly thr		
5521/1841	AAG TTC GGG GAT TTG GAT GAA CAA GAA TTT	5551/1851	GTT TAC AAG GAG CCT GCA ATA ACC AAA CTT
lys phe gly asp leu asp glu gln glu phe	val tyr lys glu pro ala ile thr lys leu		

FIG. 6A (5 of 6)

5581/1861	GCA GAG ATA TCT CAC AGA TTG GAG GGA TTT	5611/1871	TAC GGA GAA AGA TTT GGA GAG GAT GTG GTT
5641/1881	ala glu ile ser his arg leu glu gly phe	5671/1891	tyr gly glu arg phe gly glu asp val val
5701/1901	GAA GTA ATC AAA GAC TCT AAT CCT GTA GAC	5731/1911	AAG TGT AAA TTA GAT CCT AAC AAG GCA TAT
5761/1921	glu val ile lys asp ser asn pro val asp	5791/1931	lys cys lys leu asp pro asn lys ala tyr
5821/1941	ATT CAG ATT ACC TAT GTG GAG CCA TAC TTT	5851/1951	GAC ACA TAT GAG ATG AAG GAC AGA ATC ACC
5881/1961	ile gln ile thr tyr val glu pro tyr phe	5911/1971	asp thr tyr glu met lys asp arg ile thr
5941/1981	TAT TTC GAC AAA AAT TAC AAT CTT CGT CGA	5971/1991	TTC ATG TAC TGT ACA CCC TTT ACT TTA GAT
6001/2001	tyr phe asp lys asn tyr asn leu arg arg	6031/2011	phe met tyr cys thr pro phe thr leu asp
6061/2021	GGC CGT GCC CAT GGG GAA CTT CAT GAA CAA	6091/2031	TTC AAA AGG AAG ACC ATT CTG ACT ACG TCT
6121/2041	gly arg ala his gly glu leu his glu gln	6151/2051	phe lys arg lys thr ile leu thr thr ser
6181/2061	CAT GCC TTT CCT TAT ATT AAA ACA AGG GTC	6211/2071	5911/1971
6241/2081	his ala phe pro tyr ile lys thr arg val	6271/2091	AAT GTC ACT CAT AAA GAA GAG ATC ATC TTA
	5941/1981		asn val thr his lys glu glu ile ile leu
	6001/2001		5971/1991
	6061/2021		CAG AAA AAG ACA CAG GAG TTG GCA TTT GCA
	6121/2041		gln lys lys thr gln glu leu ala phe ala
	6181/2061		6031/2011
	6241/2081		CTT CAG ATG GTA CTC CAG GGA TCT GTA GGC
			leu gln met val leu gln gly ser val gly
			6091/2031
			GCC CAG GTT TTT CTG TCT GAA ATA CCT AGT
			ala gln val phe leu ser glu ile pro ser
			6151/2051
			CTG CGA CTC TGC TTT AAA GAT TTT ACT AAA
			leu arg leu cys phe lys asp phe thr lys
			6211/2071
			AGC TTA ATT GGG CCG GTT CAA AAG GAG TAT
			ser leu ile gly pro val gln lys glu tyr
			6271/2091
			CAA AGG GAA TTG GGG AAA CTA TCT TCG CCT TAA
			gln arg glu leu gly lys leu ser ser pro OCH

AGAGGCCCTACAGCCCTAGATCACAGAAAGTCCCTCAGTTATCCAAGCCAGTATTGCTTGTCCTGCCCACAGAGATTCC
 TTCAGTCGAATGAGCTTTTCGCAAAATGGATCTCTAACTGAATGCACTTGTTTTATTTCATCTGCAAAAGAGCCATGTATTC
 AACATCGAGTGTGAAAAGATCTATTGGAAACCAACATGGAATGGAATTCTGGAAATTATTATTCATTGAAGAATGCAGTG
 GCCAAGAAAATATCAAATGTAGATTGTTAACGCTTGAGAATCATGGCTATGGTTTCTAATGTTTCGGGTAACAAGCTGTTA
 TCTTTTAAGACATTTTAATGACTCAAAGGTACACTATACATTTACCATTATTTATACCATAGCTAAGGTTAAAAATTTAT
 TCACTTTAAGTTCGTATTTTTTAATTTATATCACCATTTATAGATTTCATTTTGGACCCATTTTAAATGTAGTAATGCTTA
 TTTTAAAGGTACTAAAAAATATGTGAATGTTTACCTCGTGCGGCCAGGGCCTC

FIG. 6A (6 of 6)

Allelic Variations: single nucleotide changes (polymorphisms) between hCLASP-3 cDNAs and/or genomic sequences

Isoform	Difference	Nucleotide position	Consequence
1	polymorphism	318	A to G; missense
2	polymorphism	323	A to G; Glu to Gly
3	polymorphism	2187	T to C; missense
4	polymorphism	3165	T to G; Asp to Glu

Allelic Variations: Alternative Exon usage

Isoform	Difference	Nucleotide position	Consequence
1	Exon deletion	2768-2860, inclusive	In frame deletion – 33 amino acids removed

FIG. 6B

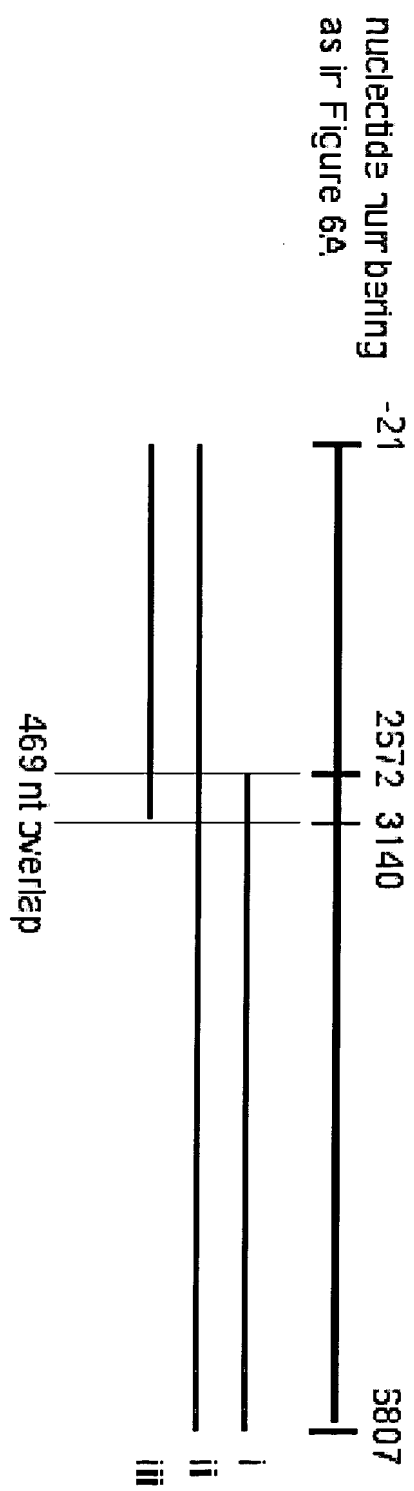


FIG. 6C

Exon 60270 - 20370

CGCCGCAGCCGCCGCCGCCGTCGCCGTCGCCGCAGCAGCCATGGCCGAGCGCCGCGCCTTCGCCCAGAAGATCAGCAGGT
AAATATCCGGCGTGGGGCGC

Exon 85360 - 85510

GTTTTTGCTTCTTCATTGTAGAACGGTGGCAGCCGAAGTTAGGAAGCAGATCTCCGGACAATATAGTGGTTCTCCCCAA
CTGCTCAAAAACCTTAATATTGTTGGCAATATATCCCATCACACCACAGTAAGTAACGTATTCAAAATATA

Exon 94500 - 94720

TCTTATCCCAACTTTTTACAAAGGTGCCCTTACCGAAGCAGTAGATCCAGTGGATTGGAAGATTACCTCATTACTCAT
CCTTTGGCTGTGGATTCTGGGCCTTTACGGGATTTGATTGAATTTCTCCAGATGATATTGAAGTTGTTTATAGTCCTCG
GGACTGCAGAACTCTGTTTCAGCTGTACCTGAAGAAAGGTAAGGAGACATTGACTTATT

Exon 94870 - 94980

TATTTTCCTTTTAAAAATAGTGAAATGGATCCACATGTTAGAGACTGTATAAGAAGTTATACAGAAGACTGGGCAATTGT
CATCAGAAAGTAAGTTATATGTTTATTACAA

Exon 100110 - 100290

ATTTATTTAACTTTTTTCTTTAATAGATATCATAAATTGGGAACAGGATTTAATCCCAATACATTAGATAAACAGAAAG
AAAGGCAAAAAGGTTTGCCAAAACAAGTTTTTTGAATCTGATGAAGCTCCAGATGGCAACAGCTACCAGGATGATCAAGTA
ATACTTTTATTCTTAAATAA

Exon 100340 - 100600

ATATTTAATGTTTTGCATGACAGGATGACCTTAAAAGACGTTCAATGTCAATAGATGATACCCAAGGGGTAGCTGGGCC
TGTAGTATCTTTGACTTGAAAAATTCACCTTCCTGATGCTTTGCTTCCAATTTACTTGATCGAACTCCAAATGAAGAAAT
AGACCGTCAGAAATGATGACCAAAGGAAATCAAACCGTCACAAAGAACTTTTTGCTTTGCATCCATCACCAGATGAGGTAT
AGATGTTTTGCATATAAAGAA

Exon 100880-101020

TTTTGGTGTGTGCTTTTCAATTTGTAGGAAGAACCAATAGAACGGCTTAGTGTTCCCTGATATACCCAAAGAACATTTTGGT
CAAAGACTTCTTGTAATAATGCTTATCACTCAAGTGAGTATTTATTTCTTTACTTACAACT

Exon 112010 – 112120

TTTTTCTTCATAAAGGTTTGAAATTGAAATTGAACCCATTTTTGCAAGTTTGGCTTTATATGATGTCAAGGAAAAGAAAA
AGGTAAGATTATATAATTTGACCATAGTTAT

Exon 113680 – 113880

AAGTTTAACATACTAATATTTTTTAGATTTTCAGAAAACTTTTATTTTGACCTTAATTCTGAGCAGATGAAAGGGTTGTTA
CGTCCACATGTACCACCTGCTGCCATTACTACCCTGGCAAGATCAGCAATTTTTCTATCACTTATCCTTCCCAAGATGT
TTTTCTTGTAATAAAGGTGAGAATAATGTTAAATATATTTG

Exon 115020-115160

TTAATCTTAACTTTTTTTGCCTTTGACAGCTAGAAAAAGTCCTACAGCAAGGAGACATTGGAGAGTGTGCAGAACCATAT
ATGATTTTCAAAGAAGCAGATGCCACCAAGGTAGAATGTTATGCTTCTCATTTCCGCCAC

Exon 117200 – 117410

ATGTATAAAGTTCTGTTTTGCAGAAATAAAGAAAACTGGAGAACTGAAGAGTCAAGCAGATCAGTTTTGCCAAAGACTT
GGGAAATATCGCATGCCTTTTGCTTGGACTGCAATCCATTTAATGAATATTGTTAGCAGTGCTGGGAGTTTGGAAAGAGA
TTCTACAGAAGTAGAAATCAGTACTGGAGGTAAGAGTGTTTCATACAAAAC

Exon 123200 - 123396

AAAATGAATTTTTTTTTTAATTCTTTGTAGAACGAAAAGGGTCTTGGTCAGAGAGGAGGAATTCTAGTATTGTTGGCAG
ACGATCACTTGAAAGGACAACAAGTGGAGATGATGCTTGTAACCTGACGAGCTTTCGACCAGCTACTCTCACAGTGACAA
ATTTTTTTAAGCAGGTATTGTTCTGTCATGTAGGAATTTT

(Next part of CLASP, starting

GAAGGAGACCGCTTAAGTGATGAAGATCTCTACAAATTCCTTGCTGATATGAGAAGGCCATCTTCTGTCTTACGGCGACT
AAGACCTATTACAG)

Exon 5560 – 5710

CTTTTTCCTCTATTATTGAAATCAGGAAGGAGACCGCTTAAGTGATGAAGATCTCTACAAATTCCTTGCTGATATGAGAA
GGCCATCTTCTGTCTTACGGCGACTAAGACCTATTACAGGTATTTAAAAATTTTGAGTAGAAATGGTTGCA

Exon 6680-6900

TTACATTGTTTTTTAATATATAATTTGCAGCTCAGCTCAAGATAGACATTTCTCCCGCACCTGAAAAATCCCCATTATTGC
CTAACTCCGGAGCTGCTTCAAGTGAAGCTTTACCCTGACAGTAGAGTTAGACCTACCAGAGAAATCTTAGAGTTTCCCGC
AAGGGATGTTTATGTTCCAAACACTACTTACAGGTAAGAGATTTTAATTTGGAGAATTCTG

Exon 38920 – 39075

GTATTTACTATCATCTATACTGTTGCTTTCACAGAAATCTTCTCTACATATACCCTCAGAGTCTTAATTTTGCCAATCGT
CAAGGTTCTGCTAGAAATATAACAGTGAAAGTCCAGTTTATGTATGGAGAGGATCCAAGCAATGCCATGCCGGTAA

hCLASP4	FKSHLESTIYTQDLHVHKFFHHCQLIQS-----GSKEVPGELIKYLKCLHAM	794
hCLASP5	IEVQAVSSVHTQDNHLEKFFTLCHSLESQVTFPIRVLDQKISEMALEHELKLSIICLNSS	715
hCLASP3	VEVVAVSSIHTQDPYLDKFFALVNALDEH-LFPVRIGDMRIMENNLENELKSSISALNSS	780
hCLASP2	ISTHLVSTVYTQDQHLHNFFQYCQKTES-----GAQALGNELVKYLKSLHAM	787
hCLASP7	VELTAVSSVHPQDPYLDKFFTLVHVLEEG-AFPFRLKDTVLSEGNVEQELRASLAALRLA	767
hCLASP1	VSTFVVSTVNTQDPHVNAFFQECQKREK-----MSQSPTS NFIRSCKNLLNVE	887
	.. *:: .** ::. ** : :.	:
hCLASP4	EIQVMIQFLPVILMQFLR-----VLTNMT-----EDDVP	824
hCLASP5	RLEPLVLFLHLVLDKLFQLSVQPMVIAGQTANFSQFAFESVVAIANSLHNSKDLQDQHG	775
hCLASP3	QLEPVVRFLHLLLDKLIILLVIRPPVIAGQIVNLGQASFEAMASIINRLHKNLEGNHDQHG	840
hCLASP2	EGHVMIAFLPTILNQFLR-----VLT-RAT-----QEEVA	816
hCLASP7	SPEPLVAFSHHVLDKLVRLVIRPPIISGQIVNLGRGAFEAMAHVSVLSVHRSLEAAQDARG	827
hCLASP1	KIHAIMSFLPIILNQFLK-----VLVQNE-----EDEIT	916
	. : : * : * : *	:
hCLASP4	INCTMV-LLHIVSKCHEEGLDS-----YLRSFIKYS-----FRPEKP	860
hCLASP5	RNCLLASVHYVFRLEPQORDVPKSGAPTALDPRSHTYGRTSAAAVSSKLLQARVMSS	835
hCLASP3	RNSLLASYIHVFRLEPNTYPNSSSPG-PGGLGGSVHYATMARSAVRPASLNLNRSRSLSN	899
hCLASP2	VNVTRV-IIHVVAQCHEEGLES-----HLRSYVKYA-----YKAEPY	852
hCLASP7	HCPQLAAVHYAFRLPGTEPSLPDGAPP---VTVQAATLARGSGRPASLYLARSKSISS	883
hCLASP1	TTVTRV-LPDIVAKCHEEQLDH-----SVQSYIKFV-----FKTRAC	952
	. . . :	:
hCLASP4	SAPQAQLIH-----ETLATTMIAILKQS-----	883
hCLASP5	SNPDLAGTHSAADEEVKNIMSSSKIADRNC SRMSYYCSGSSDAPSSPA-----	882
hCLASP3	SNPDISGTPTSPDDEVRSIIGSKGLDRSNSWNTGGPKAAPWGSNPSPSAESTQAMDRSC	959
hCLASP2	VASEYKTVH-----EELTKSMTTILKPS-----	875
hCLASP7	SNPDLAVAPGSVDDEVSRILASKLLHEELA-LQ-----	915
hCLASP1	KE---RPVH-----EDLAKNVTGLLKS-----	972
	:	:
hCLASP4	-----ADFLSINKLLKYS-----WFFFEIIAKSM	907
hCLASP5	-----APRPASKKHFEELALQ-----MUVSTGMVKSM	910
hCLASP3	NRMSSHTETSSFLQTLTGRLPTKKLFHEELALQWVVCSGSVRESALQAWFFFPMLVKSM	1019
hCLASP2	-----ADFLTSNKLLRYS-----WFFFDVLIKSM	899
hCLASP7	-----WVVSSSAVREAILQHA-----WFFFQLMVKSM	942
hCLASP1	-----DSPTVKHVLKHS-----WFFFAILKSM	995
	. * .. : ***	
	Cadherin Cleavage	
hCLASP4	ATYLLEENKIKLRRGQRFPPETYHHVLHSLLLAIIPHVTIRYAEIPDE---SRNVNYSLAS	964
hCLASP5	AQHVNMDKRDSEFRRTFRSDRFMDITTIVNVVTSEIAALLVKPKKENEQA EKMNISLAF	970
hCLASP3	VHHLVFNDKLEAPRKSRFPFERFMDDIAALVSTIASDIVSRFQKDTM---VERLNTSLAF	1076
hCLASP2	AQHLEIENSKVKLLRNQRFPPASYHHAETVVNMLMPHITQKFGDNPEA---SKNANHSLAV	956
hCLASP7	ALHLLLGQRLDTRKLRFPGRFLDDITALVGSVGLVITRVHKDVEL---AEHLNASLAF	999
hCLASP1	AQHLIDTNKIQLRRPQRFPPESYQNELDNLVMDVSDHVIWKYKDALEE---TRRATHSVAR	1052
	. : : . * ** . : . : : *	
hCLASP4	FLKRCLTLMDRGFI FNLINDYISGFSPKDP----KVLA EYKFEFLQTICNHEHYIPLNL	1019
hCLASP5	FLYDLLSLMDRGFVFNLRHYCSQLSAKLSNL---PTLISMRLEFLRILCSHEHYLNLNL	1027
hCLASP3	FLNDLLSVMDRGFVFSLIKSCYQVSSKLYSLPNPSVLVSLRLD FLRIICSHEHYVTLNL	1136
hCLASP2	FIKRCFTFMDRGFVFKQINNYISCFAPGDP----KTLFEYKFEFLRVVCNHEHYIPLNL	1011
hCLASP7	FLSDLLSLVDRGFVFSLVRAHYKQVATRLQSSPNPAALLTLRMEFTRILCSHEHYVTLNL	1059
hCLASP1	FLKRCFTFMDRGCVFKMVNNYISMFSGDL----KTL CQYKFD FLQEVQCHEHFIPCL	1107
	*: : : : * * . : *	

FIG. 8 (3 of 6)

Cadherin EC motif

hCLASP4	PMAFAKPKLQR-----VQDS--NLEYSLSDEYCKHHFLVGLLLRETSI	1060
hCLASP5	FFMNADTAPTSP--CPSISSQNSSSCSSSQDQKIASMFDLTSEYRQQHFLTGLLFTELAA	1085
hCLASP3	PCSLTTPPASPPSPSVSSATSQSSGFSTNVQDQKIANMFELSVPPFRQQHYLAGIVLTELAV	1196
hCLASP2	PMPFGKGRIQR-----YQDL--QLDYSLTDEFCRNHFLVGLLLREVGT	1052
hCLASP7	PCCPLSPPASPPSPSVSSTTSQSSTFSSQAPDPKVTSMFELSGPFRQQHFLAGILLTELAL	1119
hCLASP1	PIRSANIPDPLTP-----SES----TQELHASDMPEYSVTNEFCRKHFLIGILLREVGF	1157
	.: : : : * * : : *	
hCLASP4	ALQDN---YEIRYTAISVIKNLLIKHAFDTRYQHKNQQAQIAQLYLPFVGLLENIQRL	1116
hCLASP5	ALDAEGEGISKVQRKAVSAIHSLLSSHDLDPRCVKPEVKVKIAALYLPVGLIILDALP--	1143
hCLASP3	ILDPDAEGLFGLHKKVINMVHNLSSHSDPRYSDPQIKARVAMLYLPPLIGIMETVP--	1254
hCLASP2	ALQEFR---EVRLIAISVLKNLLIKHSFDDRYASRSHQARIATLYLPPLFGLLIENVQRI	1108
hCLASP7	ALEPEAEGAFLLHKKAISAVHSLLCGHDTDPRYAEATVKARVAELYLPPLSIARDTLP--	1177
hCLASP1	ALQEDQ---DVRHLALAVLKNLMAKHSFDDRYREPRKQAQIASLYMPLYGMLLDNMPRI	1213
	* : : : . : : : * * * : : : * * : : : :	
hCLASP4	AGRDTLYSCA-----AMPN-S----ASRDEFP CGFTSPANRGS LSTDKDTAYGS	1160
hCLASP5	-----QL-----CDFTVADTRRYRTSGSD-----	1162
hCLASP3	-----QLY-----DFTETHNQGRGPICIATDD--	1276
hCLASP2	NVRDVSPFPVNAGMTVKDESIALPA-VNPLVTPQKGSTLDNSLHKDLLGAISGIASPYTT	1167
hCLASP7	-----RLH-----DFAEGPGQSRSLASMLDSSTE	1201
hCLASP1	YLKDLYPFTVNTSNQGSRDDLSTNGGFQSQTAIKHANSVDTSFSKDVLSNIAAFSSIAIS	1273
	. :	
hCLASP4	FQ-NGHGIKREDSRGS LIPEGATGFDPDQGN TGEN-----TRQSSTRSSVSQYNRLDQYE	1213
hCLASP5	-----EEQEGAGAINQNVALAIAGNNFNLT-----SGIVLSSSLPYKQYNMLNADT	1208
hCLASP3	-----YESEGSMISQTVAMAIAGTSVPQLTR-----PGSFLLTSTSGRQHTTFSAES	1324
hCLASP2	STPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQQSSTLGNSVVRCDKLDQSE	1227
hCLASP7	-----GEGDIAGTINPSVAMAIAGGPLAPGSR-----ASISQGPPTASRAGCALSAES	1249
hCLASP1	-----TVNHADSRASLASLDSNPSTNEKSSEKTDNCEKIPRPLALIGSTLRFDRLDQAE	1327
	. : . : :	
hCLASP4	IRSLLMCYLYIVKMISED TLLTYWNKVSPQELINILILLEVCLFHF RYMGKRNIARVHDA	1273
hCLASP5	TRNLMICFLWIMKNADQSLIRKWIADLPSTQLNRILDLLFICVLCFEYKGKQSSDKVSTQ	1268
hCLASP3	SRSLLICLLWVLKNADETVLQKWFTDLSVLQNLRLDLLYLVCVSCFEYKGKVFERMNSL	1384
hCLASP2	IKSLLMCFLYILKMSDDALFTYWNKASTSELMDFFTISEVCLHQFQYMGKRYIARNQEG	1287
hCLASP7	SRTLLACVLWVLKNTTEPALLQRWATDLTLPQLGRLLDLLYLCLAAFEYKGKKA FERINSL	1309
hCLASP1	TRSLLMCFLHIMKTISYETLIAYWQRAPSPESVDFFSILDVCLQNF RYLGKRNIIRKIAA	1387
	.: : * * : : * . : : . : : : : : * : * * * :	
hCLASP4	WLSKHFGIDR-----KSQTMPALRNRSGVMQARLQHLSSLESS-----	1311
hCLASP5	VLQKSRDVKAR-----LEEALLRGE GARGEMMRRRAPGNDRFPGLNEN---	1311
hCLASP3	TFKKS KDMRAK-----LEEAILGSIGARQEMVRRSRGQLERSPSGSAFGSQ	1430
hCLASP2	LGPIVHDRKS-----QTLPVSRNRTGMMHARLQQLGSLDNS-----	1323
hCLASP7	TFKKS LDMKAR-----LEEAILGTIGARQEMVRRSRERSRSPFGNPEN----	1350
hCLASP1	AFKFVQSTQNNGT LKGSNPSCQTSGLLAQWMHSTSRHEGHKQHRSTLPIIRGKN----	1442
	. : : :	
hCLASP4	-----FTLNHSSTTTEADIFHQALLEGNTATEVSLTVLDTISFFTQC FKTQLL	1359
hCLASP5	--LRWKKEQTHWRQANEKLDKTKAE L DQEALISGNLATEAHLIILDMQENIIQASS-ALD	1368
hCLASP3	ENLRWRKDMTHWRQNT EKLDKSRAEIEHEALIDGNLATEANLIILDTLEIVQTVS-VTE	1489
hCLASP2	-----LTFNHSYGHSDADV LHQS LLEANIATEVCLTALDTLSLFTLAFKNQLL	1371
hCLASP7	--VRWRKSVTHWKQTS DRVDKTKDEMEHEALVEGNLATEASLVVLDTLEIIVQTVM-LSE	1407
hCLASP1	--ALSNPKLLQMLDNTMTS NSNEIDIVHHVDTEANIATEGCLTILDVSLFTQTQHRQLQ	1500
	. : : . : * * * * * * * . :	

FIG. 8 (4 of 6)

	ITAM	ITAM	
hCLASP4	EKFGTENVKIIQDSKVNAKELDPKYAHIQVITVVKPYFDDKELTERKTEFERNHNISRFV		1799
hCLASP5	QCFGAEFVEVIKDSTPVDKTKLDPNKAYIQITFVEPYFDEYEMKDRVTYFEKNFNLRRFM		1810
hCLASP3	ERFGEDVVEVIKDSNPVDKCKLDPNKAYIQITFVEPYFDTYEMKDRITYFDKNYNLRRFM		1932
hCLASP2	DKFGSENVKMIQDSGKVNPKDLDSKYAYIQVITHVIPFFDEKELQERKTEFERSHNIRRFM		1770
hCLASP7	ERFGDDVVEIIKDSYPVDKSKLDSQKAYIQITFVEPYFDTYELKDRVTYFDRNYGLRTFL		1851
hCLASP1	DKFGADNVKIIQDSNKNPNKDLDPKYAYIQVITVTPFFEEKEIEDRKTDFFEMHHNINRFV		1972
	: ** : *:::*** * : .**.: *::*:*. * : * : * : * : * : * :		
	ITAM	DOCK motif	
hCLASP4	FEAPYTLGSGKKQGCIEEQCKRRTILTTSNSFPYVKKRIPINCEQQINLKPIDGATDEIKD		1859
hCLASP5	YTPPFTLEGRPRGELHEQYRRNTVLTTHAFPIYIKTRISVIQKEEFVLTPIEVAIEDMCK		1870
hCLASP3	YCTPFTLDGRAHGEHQFKRKTILTTSNHFPIYIKTRVNVTHKEEIIILPIEVAIEDMQK		1992
hCLASP2	FEMPFTQTGKRQGGVEEQCKRRTILTAIHCFPIYVKKRIPVMYQHHTDLNPIEVAIDEMSK		1830
hCLASP7	FCTPFTPDGRAHGEHQHKKRKTLLSTDHAFPIYIKTRIRVCHREETVLTPIEVAIEDMQK		1911
hCLASP1	FETPFTLSGKKHGGVAEQCKRRTILTTSNHFPIYVKKRIPVISQSSTELNPIEVAIDEMSR		2032
	: * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * :		
	Coiled-coil		
hCLASP4	KTAEQLKLCSSSTDVDMIQQLKLGQVSVQVNAGPLAYARAFLNDSQASKYPPKKVSELK		1919
hCLASP5	KTLQLAVAINQEPDAKMLQMVLGQSVGATVNQGPLEVAQVFLAEIPADPKLYRHHNKLK		1930
hCLASP3	KTQELAFATHQDPADPKMLQMVLGQSVGTTVNQGPLEVAQVFLSEIPSDPKLFRHHNKLK		2052
hCLASP2	KVAELRQLCSSAEVDMIKLQKLQGSVSVQVNAGPLAYARAFLLDNTNKRYPDNKVKLLK		1890
hCLASP7	KTRELAFATEQDPPDAKMLQMVLGQSVGPTVNQGPLEVAQVFLAEIPEDPKLFRHHNKLK		1971
hCLASP1	KVSELNQLCTMEEVDMISLQKLQGSVSVKVNAGPMAYARAFLEETNAKKYPDNQVKLLK		2092
	* . : * * ** : *** * . ** ** : * : *** : . . . * :		
	Coiled-coil		
hCLASP4	DMFRKFIQACSI IALELNERLIKEDQVEYHEGLKSNFRDMVKELSDI IHEQILQEDTMHSP		1979
hCLASP5	LCFKEFIMRCGEAVEKNKRLITADQREYQ QELKKNYNKLKENLRPM IERKIPELYKPIFR		1990
hCLASP3	LCFKDFTKRCEDALRK NKSLIGPVQKEYQRELGLSSP -----		2090
hCLASP2	EVFRQFVEACGQALAVNERLIKEDQLEYQEEMKANYREMAKELSEIMHEQICPLEEKTS-		1949
hCLASP7	LCFKDFCKKCEDALRK NKALIGPDQKEYHRELERNYCRLREALQPL LTQRLPQLMAPTP-		2030
hCLASP1	EIFRQFADACGQALDVNERLIKEDQLEYQEELRSHYKDMLSELSTVMNEQITGRDDL SKR		2152
	* : . * * * : * : * : * * : * : * : *		
	PDZ ligand		
hCLASP4	WMSNTLHVFC AI SGTSSDRGYGSPRYAEV- -		2008
hCLASP5	VESQKRDSFHRSSFRKCETQLSQGS-----		2015
hCLASP3	-----		
hCLASP2	VLPNSLHIFNAISGTPTSTMVHG MTSSSSVV		1980
hCLASP7	--PGLRNSLN RASFRKADL -----		2047
hCLASP1	GVDQTCTRVISKATPALPTVSISS SAEV - -		2180

FIG. 8 (6 of 6)